

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 16:19:50 ; Search time 2330 Seconds

(without alignments)
1357.958 Million cell updates/sec

Title: US-10-658-093-19

Perfect score: 73
Sequence: 1 aacgttattatgcttttta.....tattttatttattttttt 73

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenBank1:
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2: gb_htg:*
3: gb_in:*
4: gb_om:*
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9: gb_pr:*
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13: gb_un:*
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16: em_fun:*
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33: em_htg_mus:*
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38: em_sy:*
39: em_htgo_hum:*
40: em_htgo_mus:*
41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Match	Length	DB	ID	Description
C 1	73	100.0	242	6	AX340922	AX340922 Sequence
C 2	73	100.0	245	6	AX587935	AX587935 Sequence
C 3	73	100.0	265	12	SYNINPOSP	M28858 Synthetic (
C 4	73	100.0	477	6	AX774881	AX774881 Sequence
5	73	100.0	1918	9	AK097379	AK097379 Homo sapi
6	73	100.0	2084	6	AX587848	AX587848 Sequence
7	73	100.0	2103	6	AX014320	AX014320 Sequence
8	73	100.0	2103	6	BD222199	BD222199 Human nuc
9	73	100.0	2121	9	HSM807248	BX647104 Homo sapi
10	73	100.0	3565	6	196207	196207 Sequence 44
11	73	100.0	3565	6	AX330284	AX330284 Sequence
12	73	100.0	3565	6	AX36394	AX36394 Sequence
13	73	100.0	3565	6	AX663638	AX663638 Sequence
14	73	100.0	3565	9	HSCFOS	V01512 Human cellu
15	73	100.0	4200	4	SSC132510	AJ132510 Sus scrof
16	73	100.0	5897	9	AY212879	AY212879 Homo sapi
17	73	100.0	6210	6	AX663628	AX663628 Sequence
18	73	100.0	6210	9	HOMFOS	K00650 Human fos p
19	73	100.0	135050	2	AC118536	AC118536 Canis fam
20	73	100.0	140332	2	AC118538	AC118538 Felis cat
C 21	73	100.0	168802	2	AC147196	AC147196 Sus scrof
C 22	73	100.0	174298	2	AC120514	AC120514 Bos tauru
C 23	73	100.0	181848	9	CNS07YOR	AL591403 Human chr
24	73	100.0	188938	2	AC119064	AC119064 Sus scrof
25	73	100.0	195254	2	AC117934	AC117934 Papio anu
26	73	100.0	197796	2	AC117932	AC117932 Papio anu
27	73	100.0	202267	9	DJ293M10	AF111167 Homo sapi
28	73	100.0	207930	2	AC120203	AC120203 Pan trogl
29	72	98.6	2015	4	AF540379	AF540379 Felis cat
30	71.4	97.8	402	6	AR272842	AR272842 Sequence
31	71.4	97.8	402	6	AR272850	AR272850 Sequence
32	71.4	97.8	402	6	AR276423	AR276423 Sequence
33	71.4	97.8	402	6	AR276431	AR276431 Sequence
34	71.4	97.8	402	6	AR406698	AR406698 Sequence
35	71.4	97.8	402	6	AR406706	AR406706 Sequence
36	71.4	97.8	402	6	AX062944	AX062944 Sequence
37	71.4	97.8	402	6	AX062952	AX062952 Sequence
38	71.4	97.8	402	6	AX367861	AX367861 Sequence
39	71.4	97.8	402	6	AX367869	AX367869 Sequence
40	71.4	97.8	2116	10	RNCFOSR	X06769 Rat c-fos m
41	71.4	97.8	165789	2	AC119054	AC119054 Rattus no
42	71.4	97.8	286098	2	AC121435	AC121435 Rattus no
43	69.8	95.6	6023	10	AF061881	AF061881 Mesocric
44	69.8	95.6	6210	6	AX323857	AX323857 Sequence
45	69	94.5	659	6	I24430	I24430 Sequence 2

ALIGNMENTS

RESULT 1
AX340922/c
LOCUS AX340922
DEFINITION Sequence 1169 from Patent WO0196388.
ACCESSION AX340922
VERSION AX340922.1 GI:18136904
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1
Jiang,Y., Harlocker,S.L. and Secrist,H.
TITLE Compositions and methods for the therapy and diagnosis of colon cancer

JOURNAL Patent: WO 0196388-A 1169 20-DEC-2001;
CORIXA CORPORATION (US)
FEATURES Location/Qualifiers
source 1..242
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 AACGTTTATGCTGTTTAAATTATTATTAAGATGATTCCTCAGATATTATATTTT 60
DB 190 AACGTTTATGCTGTTTAAATTATTATTAAGATGATTCCTCAGATATTATATTTT 131
CY 61 ATTTATTTT 73
DB 130 ATTTATTTT 118
RESULT 2
AX587935/c 245 bp DNA linear PAT 10-JAN-2003
LOCUS Sequence 405 from Patent WO0246467.
DEFINITION AX587935
ACCESSION AX587935
VERSION AX587935.1 GI:27656605
KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
REFERENCE 1
AUTHORS Bertucci, F., Houlgate, R., Birnbaum, D., Nguyen, C., Vicens, P. and Fert, V.
TITLE Gene expression profiling of primary breast carcinomas using arrays of candidate genes
JOURNAL Patent: WO 0246467-A 405 13-JUN-2002;
FEATURES Location/Qualifiers
source 1..245
/organism="synthetic construct"
/mol_type="unassigned DNA"
/db_xref="taxon:32630"
/note="primer"
misc_feature 1..245
/note="5' terminal sequence. v-fos fbj murine osteosarcoma viral oncogene homolog (FOS) gene."
ORIGIN
Query Match 100.0%; Score 73; DB 6; Length 245;
Best Local Similarity 100.0%; Pred. No. 0.00043;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 AACGTTTATGCTGTTTAAATTATTATTAAGATGATTCCTCAGATATTATATTTT 60
DB 180 AACGTTTATGCTGTTTAAATTATTATTAAGATGATTCCTCAGATATTATATTTT 121
CY 61 ATTTATTTT 73
DB 120 ATTTATTTT 108
RESULT 3
SYNINFOSP 265 bp mRNA linear SYN 01-JUN-1994
LOCUS Synthetic (plasmid psolif 3 fos AU-) Interferon (IFN)-beta-c-fos
DEFINITION mRNA, 3'UTR.
ACCESSION M28858
VERSION M28858.1 GI:496260
KEYWORDS interferon-beta; synthetic.
SOURCE synthetic construct
ORGANISM synthetic construct

artificial sequences.
REFERENCE 1 (bases 1 to 265)
AUTHORS Krays, V., Martin, O., Shaw, G., Deschamps, J. and Huez, G.
TITLE Translational blockade imposed by cytokine-derived UA-rich sequences
JOURNAL Science 245 (4920), 852-855 (1989)
MEDLINE 89368907
PubMed 2672333
COMMENT On Jun 4, 1994 this sequence version replaced gi:342034.
FEATURES source text: Synthetic construct mRNA.
Location/Qualifiers
source 1..265
/organism="synthetic construct"
/mol_type="mRNA"
/db_xref="taxon:32630"
1..265
/note="IFN-beta-c-fos"
3'UTR
polyA_signal
polyA_site 263
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Query Match 100.0%; Score 73; DB 12; Length 265;
Best Local Similarity 100.0%; Pred. No. 0.00042;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 AACGTTTATGCTGTTTAAATTATTATTAAGATGATTCCTCAGATATTATATTTT 60
DB 81 AACGTTTATGCTGTTTAAATTATTATTAAGATGATTCCTCAGATATTATATTTT 140
CY 61 ATTTATTTT 73
DB 141 ATTTATTTT 153
RESULT 4
AX774881/c 477 bp DNA linear PAT 09-JUL-2003
LOCUS Sequence 197 from Patent WO03038129.
DEFINITION AX774881
ACCESSION AX774881
VERSION AX774881.1 GI:32486397
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Rapont, M.
TITLE Methods for assessing and treating leukemia
JOURNAL Patent: WO 03038129-A 197 08-MAY-2003;
Ortho-Clinical Diagnostics, Inc. (US)
FEATURES Location/Qualifiers
source 1..477
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred. No. 0.00036;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
CY 1 AACGTTTATGCTGTTTAAATTATTATTAAGATGATTCCTCAGATATTATATTTT 60
DB 189 AACGTTTATGCTGTTTAAATTATTATTAAGATGATTCCTCAGATATTATATTTT 130
CY 61 ATTTATTTT 73
DB 129 ATTTATTTT 117
RESULT 5
AK097379 1918 bp mRNA linear PRI 15-JUL-2002
LOCUS AK097379

DEFINITION Homo sapiens cDNA FLJ40060 fis. clone TCOLN2000236, highly similar to P55-C-FOS PROTO-ONCOGENE PROTEIN.

ACCESSION AK097379

VERSION AK097379.1 GI:21757114

KEYWORDS oligo cloning; file (full insert sequence).

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS 1 Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T., Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuma,N., Sato,K., Tanikawa,M., Yamazaki,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Wakamatsu,A., Ishii,S., Yamamoto,U., Isono,Y., Kawai-Hio,Y., Saito,K., Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y., Sekine,M., Kikuchi,H., Murakawa,K., Kanehori,K., Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y., Sugano,S., Nagaharti,K., Masuhio,Y., Nagai,K. and Isogai,T.

TITLE NED0 human cDNA sequencing project

JOURNAL Unpublished

REFERENCES 2 (bases 1 to 1918)

AUTHORS Isogai,T. and Yamamoto,J.

TITLE Direct Submission

JOURNAL Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan (E-mail:genomc@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986) NED0 human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES

Source 1..1918

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="TCOLN2000236"

/tissue_type="colon, tumor tissue"

/clone_11b="TCOLN2"

/note="Cloning vector: pEM18FLJ3"

ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0.00024;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTTATTTATTAAGATGATTCAGATTTATTTT 60

DB 1737 AACGTTTATGCTGTTTAAATTTATTTATTAAGATGATTCAGATTTATTTT 1796

QY 61 ATTTATTTT 73

DB 1797 ATTTATTTT 1809

LOCUS AX587848 2084 bp DNA linear PAT 10-JAN-2003

DEFINITION Sequence 318 from Patent WO0246467.

ACCESSION AX587848

VERSION AX587848.1 GI:28212432

KEYWORDS

SOURCE

ORGANISM

REFERENCE

1 synthetic construct

2 synthetic construct

3 artificial sequence.

AUTHORS Bertucci,F., Houlgate,R., Birnbaum,D., Nguyen,C., Vlene,P. and

Pert,V.

TITLE Gene expression profiling of primary breast carcinomas using arrays

JOURNAL of candidate genes

PATENT: WO 0246467-A 318 13-JUN-2002;

IPSOGEN (FR)

FEATURES

Source 1..2084

Location/Qualifiers

/organism="synthetic construct"

/mol_type="unassigned DNA"

/db_xref="taxon:32630"

/note="primer"

misc_feature 1..2084

/note="y-fos fpi murine osteosarcoma viral oncogene homolog (FOS) gene."

ORIGIN

Query Match 100.0%; Score 73; DB 6; Length 2084;

Best Local Similarity 100.0%; Pred. No. 0.00023;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTTATTTATTAAGATGATTCAGATTTATTTT 60

DB 1922 AACGTTTATGCTGTTTAAATTTATTTATTAAGATGATTCAGATTTATTTT 1981

QY 61 ATTTATTTT 73

DB 1992 ATTTATTTT 1994

LOCUS AX014320 2103 bp DNA linear PAT 07-SEP-2000

DEFINITION Sequence 28 from Patent WO9954353.

ACCESSION AX014320

VERSION AX014320.1 GI:10040674

KEYWORDS

SOURCE

ORGANISM

ORGANISM Homo sapiens (human)

REFERENCE

1 Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

AUTHORS Schmitz,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and

Pilarsky,C.

TITLE Human nucleic acid sequences of normal uterus tissue

JOURNAL Patent: WO 9954353-A 28 28-OCT-1999;

SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN BERND (DE); ROSENTHAL ANDRE (DE); METZGEN GES FUER GENOMFORSCHUN (DE); PILARSKY CHRISTIAN (DE)

FEATURES

Source 1..2103

Location/Qualifiers

/organism="Homo sapiens"

/mol_type="unassigned DNA"

/db_xref="taxon:9606"

ORIGIN

Query Match 100.0%; Score 73; DB 6; Length 2103;

Best Local Similarity 100.0%; Pred. No. 0.00023;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTTATTTATTAAGATGATTCAGATTTATTTT 60

DB 1878 AACGTTTATGCTGTTTAAATTTATTTATTAAGATGATTCAGATTTATTTT 1937

QY 61 ATTTATTTT 73

DB 1938 ATTTATTTT 1950

LOCUS BD222199 2103 bp DNA linear PAT 17-JUL-2003

DEFINITION Human nucleic acid sequence originating in normal uterine tissue.

ACCESSION BD222199

VERSION BD222199.1 GI:33031969

KEYWORDS

UP 2002512017-A/28.

SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2103)
AUTHORS Specht,T., Hinzmann,B., Schmitt,A., Pilarsky,C., Dahl,E. and Rosenthal,A.
TITLE Human nucleic acid sequence originating in normal uterine tissue
JOURNAL Patent: JP 2002512017-A 28 23-APR-2002;
COMMENT METAGEN GESELLSCHAFT FUER GENOM FORSCHUNG MBH
OS Homo sapiens (human)
PN JP 2002512017-A/28
PD 23-APR-2002 JP 2000544691
PF 15-APR-1999 JP 2000544691
PR 17-APR-1998 DE 198 17 946.4
PI THOMAS SPECHT, BERND HINZMANN, ARMIN SCHMITT, CHRISTIAN PILARSKY,
PI EDGAR DAHL,
PI ANDRE ROSENTHAL,
PC C12N15/09,A61K48/00,A61P35/00,C07K14/47,C07K16/18,
PC C12N1/19,
PC C12N1/21,C12N5/00,C12P21/08,C12Q1/68,G01N33/68,C12N15/00, PC
A61K37/02,
PC C12N5/00
CC Human nucleic acid sequence originating in normal uterine tissue
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FH Key Location/Qualifiers
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FT /organism='Homo sapiens (human)'.
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Location/Qualifiers
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
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Best Local Similarity 100.0%; Pred.No.0.00023;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGTTTATGCTTTTAAATTTATTTAATGATGATTCGACATTTATTTT 60
DB 1878 AACGTTTATGCTTTTAAATTTATTTAATGATGATTCGACATTTATTTT 1937
QY 61 ATTTATTTT 73
DB 1938 ATTTATTTT 1950
RESULT 9
HSM807248 2121 bp mRNA linear PRI 30-AUG-2003
LOCUS HSM807248 Homo sapiens mRNA; cDNA DKFZp686J04124 (from clone DKFZp686J04124).
DEFINITION BX647104
ACCESSION BX647104.1 GI:34366132
VERSION
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
QY Homo sapiens
DB Homo sapiens
QY Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 2121)
Wambut,R., Heubner,D., Mewes,H.W., Weil,B., Amd,C., Osanger,A.,
Fodor,G., Han,M. and Wiemann,S.
The German Human cDNA Consortium
Submitted (27-AUG-2003) MIPS, Ingolstaedter Landstr.1, D-85764
Neuberger, GERMANY
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ), Email s.wiemann@dkfz-heidelberg.de;
sequenced by AGOWA (Berlin/Germany) within the cDNA sequencing
consortium of the German Genome Project.
This clone (DKFZp686J04124) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de Further

Information about the clone and the sequencing project is available
at <http://mips.gsf.de/proc/cDNA/>.
Location/Qualifiers
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/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/ciseq_type="human uterus"
/clone_lib="686 (synonym: h1cc3). Vector pSport1_Sfi; host
DH10B; sites SfiIA + SfiIB"
/dev_stage="adult"
2078..2083
polyA_signal
polyA_site
2102
ORIGIN
Query Match 100.0%; Score 73; DB 9; Length 2121;
Best Local Similarity 100.0%; Pred.No.0.00023;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGTTTATGCTTTTAAATTTATTTAATGATGATTCGACATTTATTTT 60
DB 1921 AACGTTTATGCTTTTAAATTTATTTAATGATGATTCGACATTTATTTT 1980
QY 61 ATTTATTTT 73
DB 1981 ATTTATTTT 1993
RESULT 10
196207 196207 3565 bp DNA linear PAT 01-DEC-1998
LOCUS 196207 Sequence 44 from patent US 5734039.
DEFINITION 196207
ACCESSION 196207
VERSION 196207.1 GI:3940677
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 3565)
AUTHORS Calabretta,B. and Skorski,T.
TITLE Antisense oligonucleotides targeting cooperating oncogenes
JOURNAL Patent: US 5734039-A 44 31-MAR-1998;
FEATURES
source Location/Qualifiers
1..3565
/organism="unknown"
/mol_type="unassigned DNA"
ORIGIN
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Best Local Similarity 100.0%; Pred.No.0.0002;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGTTTATGCTTTTAAATTTATTTAATGATGATTCGACATTTATTTT 60
DB 3353 AACGTTTATGCTTTTAAATTTATTTAATGATGATTCGACATTTATTTT 3412
QY 61 ATTTATTTT 73
DB 3413 ATTTATTTT 3425
RESULT 11
AX330284 3565 bp DNA linear PAT 09-JAN-2002
LOCUS AX330284
DEFINITION AX330284 Sequence 793 from Patent WO0194629.
ACCESSION AX330284
VERSION AX330284.1 GI:18103262
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
QY Homo sapiens
DB Homo sapiens
QY Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

```

REFERENCE          1
AUTHORS            Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
                   Horrigan,S., Soppec,D.R. and Weaver,Z.
TITLE              Cancer gene determination and therapeutic screening using signature
JOURNAL            Patent: WO 0194629-A 793 13-DEC-2001;
FEATURES            Avalon Pharmaceuticals (US)
SOURCE              Location/Qualifiers
                   1. 3565
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Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY                61 ATTTATTTTTTT 73
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DB                3413 ATTTATTTTTTT 3425
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RESULT 12
AX336394           3565 bp      DNA      linear      PAT 09-JAN-2002
LOCUS              Sequence 6903 from Patent WO0194629.
ACCESSION          AX336394
VERSION            AX336394.1 GI:18127113
KEYWORDS
SOURCE             Homo sapiens (human)
ORGANISM           Homo sapiens
REFERENCE          1
AUTHORS            Young,P.E., Augustus,M., Carter,K.C., Ebner,R., Endress,G.,
                   Horrigan,S., Soppec,D.R. and Weaver,Z.
TITLE              Cancer gene determination and therapeutic screening using signature
JOURNAL            Patent: WO 0194629-A 6903 13-DEC-2001;
FEATURES            Avalon Pharmaceuticals (US)
SOURCE              Location/Qualifiers
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                   /mol_type="unassigned DNA"
                   /db_xref="taxon:9606"

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Query Match       100.0%; Score 73; DB 6; Length 3565;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY                1 AACGTTTATGCTGTTTAAATTTATTTAATGATGATTCAGATTTATATTTT 60
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DB                3353 AACGTTTATGCTGTTTAAATTTATTTAATGATGATTCAGATTTATATTTT 3412
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QY                61 ATTTATTTTTTT 73
                   |||||||
DB                3413 ATTTATTTTTTT 3425
                   |||||||

RESULT 13
AX663638           3565 bp      DNA      linear      PAT 22-MAR-2003
LOCUS              Sequence 13 from Patent WO02097127.
ACCESSION          AX663638
VERSION            AX663638.1 GI:29163846
KEYWORDS
SOURCE             Homo sapiens (human)

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ORGANISM           Homo sapiens
REFERENCE          1
AUTHORS            Oellers,N., Gehrmann,M., Kallabis,H., Hall,R., Schlze,T. and
                   Kroegel,C.
TITLE              Genes and proteins for prevention, prediction, diagnosis, prognosis
JOURNAL            and treatment of chronic lung disease
                   Patent: WO 02097127-A 13 05-DEC-2002;
                   Bayer Aktiengesellschaft (DE)
FEATURES            Location/Qualifiers
SOURCE              1. 3565
                   /organism="Homo sapiens"
                   /mol_type="unassigned DNA"
                   /db_xref="taxon:9606"

ORIGIN
Query Match       100.0%; Score 73; DB 6; Length 3565;
Best Local Similarity 100.0%; Pred. No. 0.0002;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY                1 AACGTTTATGCTGTTTAAATTTATTTAATGATGATTCAGATTTATATTTT 60
                   |||||||
DB                3353 AACGTTTATGCTGTTTAAATTTATTTAATGATGATTCAGATTTATATTTT 3412
                   |||||||

QY                61 ATTTATTTTTTT 73
                   |||||||
DB                3413 ATTTATTTTTTT 3425
                   |||||||

RESULT 14
HSCFOS            3565 bp      DNA      linear      PRI 21-NOV-1994
LOCUS              Human cellular oncogene c-fos (complete sequence).
ACCESSION          V01512
VERSION            V01512.1 GI:29903
KEYWORDS            oncogene.
SOURCE             Homo sapiens (human)
ORGANISM           Homo sapiens
REFERENCE          1
AUTHORS            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                   Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
                   1 (bases 1 to 3565)
                   Van Straten,F., Muller,R., Curran,T., Van Bevern,C. and
                   Verma,I.M.
TITLE              Complete nucleotide sequence of a human c-onc gene: deduced amino
JOURNAL            acid sequence of the human c-fos protein
MEDLINE            Proc. Natl. Acad. Sci. U.S.A. 80 (11), 3183-3187 (1983)
PUBMED            6574479
COMMENT            Data kindly reviewed (10-OCT-1983) by F. van Straten.
FEATURES            Location/Qualifiers
SOURCE              1. 3565
                   /organism="Homo sapiens"
                   /mol_type="genomic DNA"
                   /db_xref="taxon:9606"
                   132..3515
                   /gene="c-fos"
                   132..3515
                   /gene="c-fos"
                   132..3515
                   /note="possible transcript"
                   join(132..429,1183..1434,1866..1973,2088..3239)
                   /gene="c-fos"
                   132..429
                   /gene="c-fos"
                   132..429
                   /note="(alternate start site)"
                   /number=1
                   136..3515
                   /gene="c-fos"

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Oy 61 ATTTATTTTTT 73
|||
Db 3965 ATTTATTTTTT 3977
|||

Search completed: October 14, 2004, 18:09:30
Job time : 2338 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 16:18:30 ; Search time 283 Seconds
(without alignments)
1095.825 Million cell updates/sec

Title: US-10-658-093-19

Perfect score: 73
Sequence: 1 aacgtttatcgtgtttta.....cattttatttattttttt 73

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 212409041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N Geneseq_29Jan04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2003as:*
8: geneseqn2003bs:*
9: geneseqn2003cs:*
10: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	75	6	AAD46901 C-fos 3'
2	73	100.0	242	6	ABL37580 Human col
3	73	100.0	245	6	ABV94414 Breast ca
4	73	100.0	465	8	ACH23964 Human adu
5	73	100.0	477	9	ABZ35131 Human gen
6	73	100.0	477	9	ADBE84978 Fatnsey1
7	73	100.0	1176	7	ABX62923 Human act
8	73	100.0	1918	9	ADD29870 Human tum
9	73	100.0	1918	9	ADD29870 Human tum
10	73	100.0	1946	4	AAI13509 Probe #34
11	73	100.0	1946	4	ABAS5207 Human foe
12	73	100.0	1946	4	AAI34869 Human bre
13	73	100.0	1946	4	ABA44752 Human bre
14	73	100.0	1946	4	ABA24954 Probe #34
15	73	100.0	1946	4	AAK28922 Human bon
16	73	100.0	1946	5	AAK03468 Human bra
17	73	100.0	1946	6	ABSO3451 Probe #33
18	73	100.0	2084	6	ABSO3451 Human gen
19	73	100.0	2103	6	ABV93327 Breast ca
20	73	100.0	2135	8	AAZ41352 Human nor
21	73	100.0	2164	8	ADB47308 Human cdn
22	73	100.0	2180	6	ACH04087 Human ova
23	73	100.0	2227	7	ABX62920 Human act

24	73	100.0	2461	3	AAC98119 Human col
25	73	100.0	2461	4	AAH33223 Human col
26	73	100.0	3514	6	ABKS0444 Human v-f
27	73	100.0	3565	3	AAV20466 Human c-f
28	73	100.0	3565	3	AAA34970 Human ade
29	73	100.0	3565	3	AAF21092 Human low
30	73	100.0	3565	6	AB168566 Kidney ca
31	73	100.0	3565	6	AB162456 Colon ade
32	73	100.0	3565	6	ABK84488 Human cdn
33	73	100.0	3565	6	ABK64754 Human ben
34	73	100.0	3565	7	ACC46762 Human cop
35	73	100.0	3565	7	AB296786 Human nuc
36	73	100.0	6210	2	AAO63815 c-fos gen
37	73	100.0	6210	3	AAH34969 Human ade
38	73	100.0	6210	3	AAF21091 Human low
39	73	100.0	6210	6	ABT10875 Human bre
40	73	100.0	6210	6	ABZ35089 Human gen
41	73	100.0	6210	7	ACC46752 Human cop
42	73	100.0	6210	7	ABZ96785 Human nuc
43	73	100.0	16595	3	AAH34973 Human ade
44	73	100.0	16595	3	AAF21095 Human low
45	73	100.0	16595	7	ABZ96789 Human nuc

ALIGNMENTS

RESULT 1
ID AAD46901 standard; DNA, 75 BP.
XX AAD46901;
AC AAD46901;
XX 27-JAN-2003 (first entry)
DT
XX C-fos 3' UTR ARE DNA #1.
DE
XX Gene expression; transcript stability; drug screening; AU-rich element;
KW ARE; C-fos; ds.
XX Mammalia.
OS
XX WO200272844-A1.
FN
XX 19-SEP-2002.
PD
XX 08-MAR-2002; 2002MO-AUD000351.
PF
XX 09-MAR-2001; 2001US-0274770P.
PR
XX (GENE-) GENE STREAM PTY LTD.
PA
XX Daily J;
PI
XX WPI; 2002-759847/82.
DR
XX
XX New expression vector useful for modulating gene expression, identifying
PT and analyzing regulatory sequences, new targets and reagents for treating
PT human diseases, comprises a transcribable polynucleotide encoding an RNA
PT element.
XX
XX Claim 11; Page 59; 1033p; English.
XX
XX The present invention relates to novel expression vectors and/or reporter
CC vectors providing kinetics of protein expression with improved temporal
CC correlation to the promoter activity. The expression of nucleotides encoding
CC transcribable polynucleotides having sequences of a transcript corresponding
CC to the transcribable polynucleotide. The expression vectors are useful
CC for modulating the stability of a transcript and determining expression
CC of a polynucleotide of interest. They are useful for modulating gene
CC expression, identifying and analyzing regulatory sequences, new targets
CC and reagents for treating human diseases and for drug screening. The

CC Present sequence is c-fos 3' UTR ARE (AU-rich element) DNA. This sequence
 CC is used in the exemplification of the invention

XX Sequence 75 BP; 20 A; 3 C; 7 G; 45 T; 0 U; 0 Other;

Query Match 100.0%; Score 73; DB 6; Length 75;
 Best Local Similarity 100.0%; Pred. No. 7.1e-06;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTATTTAAGATGATCTCAGATATTTATTTT 60
 DB 3 AACGTTTATGCTGTTTAAATTATTTAAGATGATCTCAGATATTTATTTT 62
 QY 61 ATTTATTTT 73
 DB 63 ATTTATTTT 75

RESULT 2

ABL37580/c
 ID ABL37580 standard; cDNA; 242 BP.

XX ABL37580;

XX 08-APR-2002 (first entry)

XX Human colon tumour antigen polynucleotide SEQ ID NO:1169.

XX Human; colon cancer; colon tumour antigen; cytostatic; vaccine;

XX colon tumour metastatic antigen; diagnosis; gene; ss.

XX Homo sapiens.

XX WO200196388-A2.

XX 20-DEC-2001.

XX 08-JUN-2001; 2001WO-US018557.

XX 09-JUN-2000; 2000US-0210899P.

XX 20-FEB-2001; 2001US-0270216P.

XX (CORI-) CORIXA CORP.

XX Jiang Y, Harlocker SL, Secret H;

XX WPI; 2002-114514/15.

XX Novel isolated colon tumor polynucleotide differentially expressed in
 PT colon tumor or colon metastatic tumor and polypeptides encoded by them,
 PT useful for inhibiting development of cancer in patient.

XX Claim 1; SEQ ID NO 1169; 105bp; English.

XX ABL36412 to ABL3645 represent human colon tumour antigen cDNA clones (I)
 CC which were isolated from human colon tumour and colon metastatic tumour
 CC cDNA libraries. (I) have cytostatic activity and can be used in vaccine
 CC production. (I) can be used for stimulating and/or expanding T cells
 CC specific for a tumour protein on contact with the T cells. They are also
 CC useful for inhibiting the development of cancer in a patient. (I) can be
 CC used as probes or primers for nucleic acid hybridisation, for preparing
 CC mutant species primers, or primers for use in genetic constructions. (I)
 CC can be used in the diagnosis of a colon tumour

XX Sequence 242 BP; 102 A; 38 C; 21 G; 78 T; 0 U; 3 Other;

Query Match 100.0%; Score 73; DB 6; Length 242;

Best Local Similarity 100.0%; Pred. No. 6.2e-06;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTATTTAAGATGATCTCAGATATTTATTTT 60
 DB 190 AACGTTTATGCTGTTTAAATTATTTAAGATGATCTCAGATATTTATTTT 131

QY 61 ATTTATTTT 73

DB 130 ATTTATTTT 118

RESULT 3

ABV94414/c
 ID ABV94414 standard; cDNA; 245 BP.

XX ABV94414;

XX 08-JAN-2003 (first entry)

XX Breast carcinoma related nucleotide sequence SEQ ID NO:405.

XX Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;
 XX ss.

XX Homo sapiens.

XX WO200246467-A2.

XX 13-JUN-2002.

XX 07-DEC-2001; 2001WO-IB002811.

XX 08-DEC-2000; 2000US-0254090P.

XX 07-DEC-2001; 2001US-00007926.

XX (IPSO-) IPSOGEN.

XX Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Vians P, Felt V;

XX WPI; 2002-619023/66.

XX Novel polynucleotide library useful in molecular characterization of a
 PT carcinoma, comprising a pool of polynucleotide sequences or its
 PT subsequences which are either underexpressed or overexpressed in tumor
 PT cells.

XX Claim 1; Page 364; 401bp; English.

XX The present invention describes a polynucleotide library (I) useful in
 CC the molecular characterization of a carcinoma, comprising a pool of
 CC polynucleotides or its subsequences which are either underexpressed or
 CC overexpressed in tumour cells, and correspond to any of the
 CC polynucleotide sequences chosen from the 468 sequences given in ABV94010
 CC to ABV94477. Also described: (1) a polynucleotide array (II) useful for
 CC the prognosis or diagnostic of tumour, comprising (I); and (2) detecting
 CC (MI) differentially expressed polynucleotide sequences which are
 CC correlated with a cancer, involves obtaining a polynucleotide sample from
 CC a patient, and reacting the polynucleotide sample obtained with a probe
 CC immobilised on a solid support, where the probe comprises any combination
 CC of the polynucleotide sequences of (I) or its expression products encoded
 CC by polynucleotide sequences of (I), and detecting the reaction product.
 CC (I) have cytostatic activities and can be used as anti-tumour agents. (I)
 CC is useful in molecular characterisation of a carcinoma. (I) and (II) are
 CC useful for the prognosis or diagnostic of tumour, in differentiating a
 CC normal cell from a cancer cell, detecting a hormone sensitive tumour
 CC cell, differentiating a tumour with lymph nodes from a tumour without
 CC lymph nodes, differentiating anticycline-sensitive tumours from
 CC antacycline-insensitive tumours, and classifying good and poor prognosis
 CC primary breast tumours. (I) is useful for large-scale molecular
 CC characterisation of breast cancer that help in prediction, prognosis and
 CC cancer treatment, and for detecting differentially expressed genes that
 CC correlated with a cancer

XX Sequence 245 BP; 101 A; 40 C; 25 G; 72 T; 0 U; 7 Other;

Query Match 100.0%; Score 73; DB 6; Length 245;

Best Local Similarity 100.0%; Pred. No. 6.2e-06;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTATGCTGTTTAAATTATTTATTAAGATGATCTCAGATATTATATTTT 60
DB 180 AACGTTATGCTGTTTAAATTATTTATTAAGATGATCTCAGATATTATATTTT 121
QY 61 ATTTTATTTT 73
DB 120 ATTTTATTTT 108

RESULT 4
ACH22964
ID ACH22964 standard; cDNA; 465 BP.
XX
AC ACH22964;
XX
DT 13-OCT-2003 (first entry)
XX
DE Human adult ovary cDNA #1344.
XX
KW Human; ss; sequencing by hybridisation; SBH; expressed sequence tag; EST;
KW genome mapping; biodiversity; genetic disorder.
XX
OS Homo sapiens.
XX
PN US2003073623-A1.
XX
PD 17-APR-2003.
XX
PF 30-JUL-2001; 2001US-00918995.
XX
PR 30-JUL-2001; 2001US-00918995.
XX
XX (DRMA/) DRMANAC R T.
XX (LABA/) LABAT I.
XX (SPAC/) STACHE-CRAIN B.
XX (DICK/) DICKSON M C.
XX (JONE/) JONES L W.
XX
PI Dmanac RT, Labat I, Stache-Crain B, Dickson MC, Jones LM;
XX
XX WPI; 2003-615964/58.
XX
PT New polynucleotide sequences obtained from various cDNA libraries, useful
PT as hybridization probes, as oligomers for PCR, for chromosome and gene
PT mapping, in the recombinant production of protein, or in generating
PT antisense DNA or RNA.
XX
XX Claim 1; SEQ ID NO 10176; 44pp; English.
XX
XX The invention relates to an isolated polynucleotide comprising any one of
XX 38043 cDNA sequences, appearing as ACH2789-ACH50831, whose sequence was
XX determined by the technique of SBH (sequencing by hybridisation). Also
XX included is a purified polypeptide comprising a sequence corresponding to
XX a reading frame of the novel polynucleotide. The nucleic acid sequences
XX are useful in diagnostics as expressed sequence tags (EST) for
XX identifying expressed genes or for physical mapping of the human genome,
XX in forensics, in assessing biodiversity, or in identifying mutations
XX responsible for genetic disorders and other traits. The nucleotide
XX sequences are also useful as hybridisation probes, as oligomers for PCR,
XX for chromosome and gene mapping, in the recombinant production of
XX protein, or in generating antisense DNA or RNA. The purified polypeptide
XX is useful for generating antibodies specific for it. The present sequence
XX is one of the 38043 isolated cDNA/EST sequences. Note: The sequence data
XX for this patent did not form part of the printed specification, but was
XX obtained in electronic format directly from USPTO at
XX seqdata.uspto.gov/sequence.html?docID=20030073623
XX
XX Sequence 465 BP; 146 A; 58 C; 74 G; 169 T; 0 U; 18 Other;
XX
Query Match 100.0%; Score 73; DB 8; Length 465;
Best Local Similarity 100.0%; Pred. No. 5.8e-06;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTATGCTGTTTAAATTATTTATTAAGATGATCTCAGATATTATATTTT 60
DB 207 AACGTTATGCTGTTTAAATTATTTATTAAGATGATCTCAGATATTATATTTT 266
QY 61 ATTTTATTTT 73
DB 267 ATTTTATTTT 279

RESULT 5
ABZ35131/c
ID ABZ35131 standard; cDNA; 477 BP.
XX
AC ABZ35131;
XX
DT 05-FEB-2003 (first entry)
XX
DE Human gene expression profile polynucleotide SEQ ID NO 243.
XX
XX Human; artery; endothelium; umbilical; vein; aorta; pulmonary artery;
KW bronchial epithelium; prostate; muscle; lung fibroblast; osteoblast;
KW tumour; microarray; genome mapping; antibiotic; antiviral; antifungal;
KW gene expression; gene; ss.
XX
OS Homo sapiens.
XX
PN WO200274979-A2.
XX
PN 26-SEP-2002.
XX
PF 20-MAR-2002; 2002WO-US008456.
XX
PR 20-MAR-2001; 2001US-0276947P.
XX
XX (OROTH) ORTHO CLINICAL DIAGNOSTICS INC.
XX
XX Wan Y, Wang Y;
XX
XX WPI; 2002-740862/80.
XX
XX New gene expression profile generated from primary, endothelial,
PT epithelial, and muscle cell types, useful for identifying disease
PT pathologies involving alterations of gene expression, e.g. cancer.
XX
XX Claim 7; Page 427; 850pp; English.
XX
XX The invention relates to a gene expression profile comprising one or more
XX genes (ABZ34889-ABZ35692) and generated from a cell type. The cell type
XX is a coronary artery endothelium, umbilical artery or vein endothelium,
XX aortic endothelium, dermal microvascular endothelium, pulmonary artery
XX endothelium, myocardium microvascular endothelium, keratinocyte
XX epithelium, bronchial epithelium, mammary epithelium, prostate
XX epithelium, renal cortical epithelium, renal proximal tubule epithelium,
XX small airway epithelium, renal epithelium, umbilical artery smooth
XX muscle, neonatal dermal fibroblast, pulmonary artery smooth muscle,
XX dermal fibroblast, neural progenitor cells, skeletal muscle, astrocytes,
XX aortic smooth muscle, mesangial cells, coronary artery smooth muscle,
XX bronchial smooth muscle, uterine smooth muscle, lung fibroblast,
XX osteoblasts or prostate stromal cell. The gene expression profile is used
XX for determining the level of RNA expression for a sample, determining the
XX phenotype of a cell and distinguishing cell types. The gene or a protein
XX expression profile is useful in identifying disease pathologies involving
XX alterations of gene expression. The assessment of expression profiles may
XX provide meaningful information with respect to tumour type and stage
XX treatment methods, and prognosis. The gene or protein expression profile
XX may also be used for creating microarrays. The microarray is useful for
XX genetic and physical mapping of genomes, DNA sequencing, genetic or
XX medical diagnosis, genotyping of organisms, confirming cell or tissue
XX identifications and in identifying promising antibiotics, antiviral or
XX antifungal agents
XX
XX Sequence 477 BP; 188 A; 85 C; 59 G; 144 T; 0 U; 1 Other;


```

XX  MO200157277-A2.
XX
XX  09-AUG-2001.
XX
XX  30-JAN-2001; 2001WO-US000669.
XX
XX  04-FEB-2000; 2000US-0180312P.
XX  26-MAY-2000; 2000US-0207456P.
XX  30-JUN-2000; 2000US-00608408.
XX  03-AUG-2000; 2000US-00633366.
XX  21-SEP-2000; 2000US-0234687P.
XX  27-SEP-2000; 2000US-0236359P.
XX  04-OCT-2000; 2000GB-00024263.
XX
XX  (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX  Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX  WPI; 2001-483447/52.
XX
XX  Human genome-derived single exon nucleic acid probes useful for analyzing
XX  gene expression in human fetal liver.
XX
XX  Claim 1; SEQ ID NO 3512; 639bp + Sequence Listing; English.
XX
XX  The invention relates to a single exon nucleic acid probe for measuring
XX  human gene expression in a sample derived from human foetal liver. The
XX  single exon nucleic acid probes may be used for predicting, measuring and
XX  displaying gene expression in samples derived from human fetal liver. The
XX  present sequence is a single exon nucleic acid probe of the invention.
XX  Note: The sequence data for this patent did not form part of the printed
XX  specification, but was obtained in electronic format directly from WIPO
XX  at ftp.wipo.int/pub/published_pct_sequences
XX
XX  Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 U; 0 Other;
XX
SQ
Query Match      100.0%; Score 73; DB 4; Length 1946;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY  1 AACGTTTATGTTGTTTAAATTTATTTAATTAAGATGATGATTCACAGATTTATATTTT 60
DB  1579 AACGTTTATGTTGTTTAAATTTATTTAATTAAGATGATGATTCACAGATTTATATTTT 1638
OY  61 ATTTATTTT 73
DB  1639 ATTTATTTT 1651

RESULT 11
AA134869
ID  AA134869 standard; DNA; 1946 BP.
XX
XX  AA134869;
XX
XX  17-OCT-2001 (first entry)
XX
XX  Probe #3555 used to measure gene expression in human placenta sample.
XX
XX  Probe; microarray; human; placenta; antenatal diagnosis;
XX  genetic disorder; ss.
XX
XX  Homo sapiens.
XX  WO200157272-A2.
XX
XX  09-AUG-2001.
XX
XX  30-JAN-2001; 2001WO-US000663.
XX
XX  04-FEB-2000; 2000US-0180312P.
XX  26-MAY-2000; 2000US-0207456P.

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PR  30-JUN-2000; 2000US-00608408.
PR  03-AUG-2000; 2000US-00632366.
PR  21-SEP-2000; 2000US-0234687P.
PR  27-SEP-2000; 2000US-0236359P.
PR  04-OCT-2000; 2000GB-00024263.
XX
XX  (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX  Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX  WPI; 2001-488897/53.
XX
XX  Human genome-derived single exon nucleic acid probes useful for analyzing
XX  gene expression in human placenta.
XX
XX  Claim 25; SEQ ID NO 3555; 654bp; English.
XX
XX  The present invention relates to single exon nucleic acid probes (SENP).
XX  The present sequence is one such probe. The probes are useful for
XX  producing a microarray for predicting, measuring and displaying gene
XX  expression in samples derived from human placenta. The probes are useful
XX  for antenatal diagnosis of human genetic disorders
XX
XX  Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 U; 0 Other;
XX
SQ
Query Match      100.0%; Score 73; DB 4; Length 1946;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY  1 AACGTTTATGTTGTTTAAATTTATTTAATTAAGATGATGATTCACAGATTTATATTTT 60
DB  1579 AACGTTTATGTTGTTTAAATTTATTTAATTAAGATGATGATTCACAGATTTATATTTT 1638
OY  61 ATTTATTTT 73
DB  1639 ATTTATTTT 1651

RESULT 12
ABA44752
ID  ABA44752 standard; DNA; 1946 BP.
XX
XX  ABA44752;
XX
XX  01-FEB-2002 (first entry)
XX
XX  Human breast cell single exon nucleic acid probe #3447.
XX
XX  Human; microarray; single exon probe; gene expression; breast; disease;
XX  cancer; ss.
XX
XX  Homo sapiens.
XX  WO200157271-A2.
XX
XX  09-AUG-2001.
XX
XX  30-JAN-2001; 2001WO-US000662.
XX
XX  04-FEB-2000; 2000US-0180312P.
XX  26-MAY-2000; 2000US-0207456P.
XX  30-JUN-2000; 2000US-00608408.
XX  03-AUG-2000; 2000US-00632366.
XX  21-SEP-2000; 2000US-0234687P.
XX  27-SEP-2000; 2000US-0236359P.
XX  04-OCT-2000; 2000GB-00024263.
XX
XX  (MOLE-) MOLECULAR DYNAMICS INC.
XX
XX  Penn SG, Hanzel DK, Chen W, Rank DR;
XX
XX  WPI; 2001-496933/54.
XX

```

PT New spatially-addressable set of single exon nucleic acid probes, useful
 PT for measuring gene expression in sample derived from human breast,
 PT comprises number of single exon nucleic acid probes.

PS Claim 1; SEQ ID NO 3447; 327bp + Sequence Listing; English.

XX The invention relates to a spatially-addressable set of single exon
 CC nucleic acid probes for measuring gene expression in a sample derived
 CC from human breast and BT 474 cells. The method involves contacting the
 CC probes with a collection of detectably labelled nucleic acids derived
 CC from mRNA of human breast, and then measuring the label bound to each
 CC probe of the microarray. The probes are useful for verifying the
 CC expression of regions of genomic DNA predicted to encode proteins. They
 CC are useful for gene discovery, and for determining predisposition and/or
 CC prognosing breast disease. Gene expression analysis is useful for
 CC assessing the toxicity of chemical agents on cells. The microarray of
 CC this invention presents a far greater diversity of probes for measuring
 CC gene expression, with far less bias than expressed sequence tag
 CC microarrays. The method is suitable for rapid production of functional
 CC information from genomic sequence. The present sequence is a single exon
 CC nucleic acid probe of the invention. Note: The sequence data for this
 CC patent did not form part of the printed specification, but was obtained
 CC in electronic format directly from WIPO at
 CC ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 U; 0 Other;

Query Match 100.0%; Score 73; DB 4; Length 1946;

Best Local Similarity 100.0%; Pred. No. 5e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATTGCTTTTAAATTATTTAAGATGATTCAGATATTATTTT 60
 DB 1579 AACGTTTATTGCTTTTAAATTATTTAAGATGATTCAGATATTATTTT 1638

QY 61 ATTTATTTTTTT 73
 DB 1639 ATTTATTTTTTT 1651

RESULT 13

ABA24954
 ID ABA24954 standard; DNA; 1946 BP.

XX ABA24954;

XX 23-JAN-2002 (first entry)

XX Probe #3420 for gene expression analysis in human heart cell sample.

XX Human; gene expression; heart; microarray; vascular system; probe;
 KW cardiovascular disease; hypertension; cardiac arrhythmia;

KW congenital heart disease; ss.

XX Homo sapiens.

OS MO200157274-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000666.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLB-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488899/53.

XX Single exon nucleic acid probes for analyzing gene expression in human
 PT hearts.

PS Claim 1; SEQ ID NO 3420; 530bp; English.

XX The present invention relates to single exon nucleic acid probes for
 CC measuring human gene expression in a sample derived from human heart. The
 CC present sequence is one such probe. The probes may be used for
 CC predicting, measuring and displaying gene expression in samples derived
 CC from the human heart via microarrays. By measuring gene expression, the
 CC probes are useful for predicting, diagnosing, grading, staging,
 CC monitoring and prognosing diseases of the human heart and vascular system
 CC e.g. cardiovascular disease, hypertension, cardiac arrhythmias and
 CC congenital heart disease. Note: The sequence data for this patent did not
 CC form part of the printed specification, but was obtained in electronic
 CC format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences

XX Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 U; 0 Other;

Query Match 100.0%; Score 73; DB 4; Length 1946;

Best Local Similarity 100.0%; Pred. No. 5e-06; Mismatches 0; Indels 0; Gaps 0;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATTGCTTTTAAATTATTTAAGATGATTCAGATATTATTTT 60
 DB 1579 AACGTTTATTGCTTTTAAATTATTTAAGATGATTCAGATATTATTTT 1638

QY 61 ATTTATTTTTTT 73
 DB 1639 ATTTATTTTTTT 1651

RESULT 14

AAK28922
 ID AAK28922 standard; DNA; 1946 BP.

XX AAK28922;

XX 06-NOV-2001 (first entry)

XX Human bone marrow expressed single exon probe SEQ ID NO: 3479.

XX Human; bone marrow expressed exon; gene expression analysis; probe;
 KW microarray; cancer; leukaemia; lymphoma; myeloma; ss.

XX Homo sapiens.

OS MO200157276-A2.

XX 09-AUG-2001.

XX 30-JAN-2001; 2001WO-US000668.

XX 04-FEB-2000; 2000US-0180312P.

XX 26-MAY-2000; 2000US-0207456P.

XX 30-JUN-2000; 2000US-00608408.

XX 03-AUG-2000; 2000US-00632366.

XX 21-SEP-2000; 2000US-0234687P.

XX 27-SEP-2000; 2000US-0236359P.

XX 04-OCT-2000; 2000GB-00024263.

XX (MOLB-) MOLECULAR DYNAMICS INC.

XX Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-488900/53.

XX Human genome-derived single exon nucleic acid probes useful for analyzing
 PT gene expression in human bone marrow.

```

PS      Example 4; SEQ ID NO 3479; 658bp + Sequence Listing; English.
XX
CC      The present invention provides a number of single exon nucleic acid
CC      probes which are derived from genomic sequences expressed in the human
CC      bone marrow. They can be used to measure gene expression in bone marrow
CC      samples, which may enable the improved diagnosis and treatment of cancers
CC      such as lymphoma, leukemia and myeloma. The present sequence is one of
CC      the probes of the invention
XX
SQ      Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 U; 0 Other;
Query Match      100.0%; Score 73; DB 4; Length 1946;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AACGTTTATGCTGTTTAAATTATTTAATTAAGATGATTCGACGATTTATTTT 60
DB      1579 AACGTTTATGCTGTTTAAATTATTTAATTAAGATGATTCGACGATTTATTTT 1638
QY      61 ATTTATTTT 73
DB      1639 ATTTATTTT 1651

RESULT 15
AAK03468
ID      AAK03468 standard; DNA; 1946 BP.
XX
AC      AAK03468;
XX
XX      05-NOV-2001 (first entry)
DT
XX      Human brain expressed single exon probe SEQ ID NO: 3459.
DE
XX      Human; brain expressed exon; gene expression analysis; probe; microarray;
KW      Alzheimer's disease; multiple sclerosis; schizophrenia; epilepsy; cancer;
KM      88.
XX      Homo sapiens.
OS
XX      WO200157275-A2.
FN
XX      09-AUG-2001.
PD
XX      30-JAN-2001; 2001WO-US000667.
PE
XX      04-FEB-2000; 2000US-0180312P.
PR      26-MAY-2000; 2000US-0207456P.
PR      30-JUN-2000; 2000US-00608408.
PR      03-AUG-2000; 2000US-00632366.
PR      21-SEP-2000; 2000US-0234687P.
PR      27-SEP-2000; 2000US-0236359P.
PR      04-OCT-2000; 2000GB-00024263.
XX
XX      (MOLE-) MOLECULAR DYNAMICS INC.
PA
XX      Penn SG, Hanzel DK, Chen W, Rank DR;
PI
XX      WPI; 2001-483446/52.
DR
XX      Single exon nucleic acid probes for analyzing gene expression in human
XX      brains.
PS      Example 4; SEQ ID NO 3459; 650bp + Sequence Listing; English.
XX
CC      The present invention provides a number of single exon nucleic acid
CC      probes which are derived from genomic sequences expressed in the human
CC      brain. They can be used to measure gene expression in brain cell samples,
CC      which may enable the diagnosis and improved treatment of nervous system
CC      diseases such as Alzheimer's disease, multiple sclerosis, schizophrenia,
CC      epilepsy and cancers. The present sequence is one of the probes of the
CC      invention
XX

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```

SQ      Sequence 1946 BP; 482 A; 440 C; 476 G; 548 T; 0 U; 0 Other;
Query Match      100.0%; Score 73; DB 4; Length 1946;
Best Local Similarity 100.0%; Pred. No. 5e-06;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY      1 AACGTTTATGCTGTTTAAATTATTTAATTAAGATGATTCGACGATTTATTTT 60
DB      1579 AACGTTTATGCTGTTTAAATTATTTAATTAAGATGATTCGACGATTTATTTT 1638
QY      61 ATTTATTTT 73
DB      1639 ATTTATTTT 1651

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Search completed: October 14, 2004, 17:30:27
Job time : 288 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 17:26:59 ; Search time 59 Seconds

(without alignments)
686.634 Million cell updates/sec

Title: US-10-658-093-19

Perfect score: 73
Sequence: 1 aacgttttttgcgttttta.....tattttattttttttt 73Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 200000000Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents NA:*

- 1: /cgnt2_6/prodata/2/ina/5A_COMB.seq:*
- 2: /cgnt2_6/prodata/2/ina/5B_COMB.seq:*
- 3: /cgnt2_6/prodata/2/ina/6A_COMB.seq:*
- 4: /cgnt2_6/prodata/2/ina/6B_COMB.seq:*
- 5: /cgnt2_6/prodata/2/ina/6C_COMB.seq:*
- 6: /cgnt2_6/prodata/2/ina/backfile1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	73	100.0	3565	1 US-08-306-691B-44	Sequence 44, Appl
2	73	100.0	3565	5 PCT-US93-06251-20	Sequence 20, Appl
3	71.4	97.8	402	4 US-09-702-705-571	Sequence 571, App
4	71.4	97.8	402	4 US-09-702-705-579	Sequence 579, App
5	71.4	97.8	402	4 US-09-736-457-571	Sequence 571, App
6	71.4	97.8	402	4 US-09-736-457-579	Sequence 579, App
7	71.4	97.8	402	4 US-09-614-124B-571	Sequence 571, App
8	71.4	97.8	402	4 US-09-614-124B-579	Sequence 579, App
9	71.4	97.8	402	4 US-09-671-325-571	Sequence 571, App
10	71.4	97.8	402	4 US-09-671-325-579	Sequence 579, App
11	71.4	97.8	402	4 US-09-589-184-571	Sequence 579, App
12	71.4	97.8	402	4 US-09-589-184-579	Sequence 579, App
13	69	94.5	69	1 US-08-146-421-2	Sequence 2, Appl
14	40	54.8	68	4 US-09-320-609-3	Sequence 3, Appl
15	37.8	51.8	6040	4 US-10-204-708-70	Sequence 70, Appl
16	36.2	49.6	5476	4 US-10-204-708-82	Sequence 82, Appl
17	35.8	49.0	196	4 US-09-644-460-40	Sequence 40, Appl
18	35.4	48.5	2621	2 US-08-553-619B-8	Sequence 8, Appl
19	35.4	48.5	5455	4 US-10-204-708-34	Sequence 34, Appl
20	35.4	48.5	9347	4 US-10-204-708-35	Sequence 35, Appl
21	34.8	47.7	1664976	4 US-08-916-421B-1	Sequence 1, Appl
22	34.6	47.4	10467	4 US-10-204-708-2	Sequence 2, Appl
23	34.6	47.4	10482	4 US-09-322-478-23	Sequence 23, Appl
24	34.4	47.1	1190	4 US-09-390-207-1	Sequence 1, Appl
25	34.4	47.1	5562	4 US-10-204-708-63	Sequence 63, Appl
26	34.4	47.1	6040	4 US-10-204-708-69	Sequence 69, Appl
27	34.4	47.1	6243	2 US-09-056-075-1	Sequence 1, Appl

28	34.4	47.1	8607	4 US-10-204-708-71	Sequence 71, Appl
29	34.4	47.1	10467	4 US-10-204-708-1	Sequence 1, Appl
30	34.4	47.1	51719	4 US-09-918-686-2	Sequence 2, Appl
31	34.4	47.1	92139	4 US-09-918-686-1	Sequence 1, Appl
32	34.2	46.8	351	4 US-09-621-976-16138	Sequence 16138, A
33	34.2	46.8	62804	4 US-09-800-960-3	Sequence 3, Appl
34	34.2	46.8	62804	4 US-10-096-960-3	Sequence 3, Appl
35	34	46.6	2663	1 US-08-136-743B-3	Sequence 3, Appl
36	33.8	46.3	787	4 US-09-621-976-1878	Sequence 1878, Ap
37	33.8	46.3	1683	3 US-09-347-803-11	Sequence 11, Appl
38	33.8	46.3	6306	4 US-10-204-708-50	Sequence 50, Appl
39	33.8	46.3	6801	4 US-10-204-708-62	Sequence 62, Appl
40	33.8	46.3	11049	4 US-10-204-708-24	Sequence 24, Appl
41	33.6	46.0	8961	4 US-10-204-708-80	Sequence 80, Appl
42	33.6	46.0	19124	2 US-08-487-826B-13	Sequence 13, Appl
43	33.4	45.8	212	4 US-09-621-976-1325	Sequence 1325, Ap
44	33.4	45.8	268	4 US-09-621-976-73	Sequence 73, Appl
45	33.4	45.8	970	4 US-09-833-381-1294	Sequence 1294, Ap

ALIGNMENTS

RESULT 1
US-08-306-691B-44
Sequence 44, Application US/08306691B
Patent No. 5734039
GENERAL INFORMATION:
APPLICANT: Calabretta, Bruno
TITLE OF INVENTION: ANTISENSE
TITLE OF INVENTION: OLIGONUCLEOTIDES TARGETING COOPERATING ONCOGENES
NUMBER OF SEQUENCES: 55
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seidel, Gonda, Lavorgna & Monaco, P.C.
STREET: Two Penn Center, Suite 1800
CITY: Philadelphia
STATE: Pennsylvania
COUNTRY: U.S.A.
ZIP: 19102
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.50 inch, 720 Kb
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WordPerfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/306,691B
FILING DATE: September 15, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Monaco, Daniel A.
REGISTRATION NUMBER: 30,480
REFERENCE/DOCKET NUMBER: 8321-8
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-8383
TELEFAX: (215) 568-5549
TELEX: No. 5734039e
INFORMATION FOR SEQ ID NO: 44:
SEQUENCE CHARACTERISTICS:
LENGTH: 3565 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
US-08-306-691B-44

Query Match 100.0%; Score 73; DB 1; Length 3565;
Best Local Similarity 100.0%; Pred. No. 1.4e-08;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGTTTATGTTGTTTAAATTATTAATTAAGATGATTCACAGATTTATATTTT 60

Db 3353 AACGTTTATGCTTTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTT 3412

QY 61 ATTTATTTT 73

Db 3413 ATTTATTTT 3425

RESULT 2
PCT-US93-06251-20

; Sequence 20, Application PC/US9306251

; GENERAL INFORMATION:

; APPLICANT: Wickstrom, Eric and Rife, Jason P.

; TITLE OF INVENTION: Trivalent Synthesis of Oligonucleotides Containing

; NUMBER OF SEQUENCES: 93

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: SCULLY, SCOTT, MURPHY & PRESSER

; STREET: 400 Garden City Plaza

; CITY: Garden City

; STATE: NY

; COUNTRY: USA

; ZIP: 11530

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patentln Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/06251

; FILING DATE: 19930630

; CLASSIFICATION:

; ATTORNEY/AGENT INFORMATION:

; NAME: Digilio, Frank S.

; REGISTRATION NUMBER: 31,346

; REFERENCE/DOCKET NUMBER: 8586

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 516-742-4343

; TELEFAX: 516-742-4366

; TELEEX: 230 901 SAMS UR

; INFORMATION FOR SEQ ID NO: 20:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 3565 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

; MOLECULE TYPE: DNA (genomic)

; PCT-US93-06251-20

Query Match 100.0%; Score 73; DB 5; Length 3565;

Best Local Similarity 100.0%; Pred. No. 1.4e-08;

Matches 73; Conservative 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTT 60

Db 3353 AACGTTTATGCTTTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTT 3412

QY 61 ATTTATTTT 73

Db 3413 ATTTATTTT 3425

RESULT 3
US-09-702-705-571

; Sequence 571, Application US/09702705

; Patent No. 6504010

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darrick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.478C14

; CURRENT APPLICATION NUMBER: US/09/702,705

; CURRENT FILING DATE: 2000-10-30

; NUMBER OF SEQ ID NOS: 1833

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 571

; LENGTH: 402

; TYPE: DNA

; ORGANISM: Homo sapien

; US-09-702-705-571

Query Match 97.8%; Score 71.4; DB 4; Length 402;

Best Local Similarity 98.6%; Pred. No. 3.4e-08;

Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTT 60

Db 225 AACGTTTATGCTTTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTT 284

QY 61 ATTTATTTT 73

Db 285 ATTTATTTT 297

RESULT 4
US-09-702-705-579

; Sequence 579, Application US/09702705

; Patent No. 6504010

; GENERAL INFORMATION:

; APPLICANT: Wang, Tongtong

; APPLICANT: Bangur, Chaitanya S.

; APPLICANT: Lodes, Michael A.

; APPLICANT: Fanger, Gary

; APPLICANT: Vedvick, Tom

; APPLICANT: Carter, Darrick

; APPLICANT: Retter, Marc

; APPLICANT: Mannion, Jane

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND

; FILE REFERENCE: 210121.478C14

; CURRENT APPLICATION NUMBER: US/09/702,705

; CURRENT FILING DATE: 2000-10-30

; NUMBER OF SEQ ID NOS: 1833

; SOFTWARE: FastSeq for Windows Version 3.0

; SEQ ID NO 579

; LENGTH: 402

; TYPE: DNA

; ORGANISM: Homo sapien

; US-09-702-705-579

Query Match 97.8%; Score 71.4; DB 4; Length 402;

Best Local Similarity 98.6%; Pred. No. 3.4e-08;

Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTT 60

Db 225 AACGTTTATGCTTTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTT 284

QY 61 ATTTATTTT 73

Db 285 ATTTATTTT 297

RESULT 5
US-09-736-457-571

; Sequence 571, Application US/09736457

; Patent No. 6509448

```

; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Pan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-571

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Query Match          97.8%; Score 71.4; DB 4; Length 402;
Best Local Similarity 98.6%; Pred. No. 3.4e-08;
Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 AACGTTTATGCTTTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTATTTT 60
Db 225 AACGTTTATGCTTTTATTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTATTTT 284

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QY 61 ATTTATTTTGT 73
Db 285 ATTTATTTGTTT 297

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RESULT 6
US-09-736-457-579
; Sequence 579, Application US/09736457
; Patent No. 6509448
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Pan, Liqun
; APPLICANT: Wang, Aijun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C15
; CURRENT APPLICATION NUMBER: US/09/736,457
; CURRENT FILING DATE: 2000-12-13
; NUMBER OF SEQ ID NOS: 1864
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 579
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-736-457-579

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Query Match          97.8%; Score 71.4; DB 4; Length 402;
Best Local Similarity 98.6%; Pred. No. 3.4e-08;
Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 AACGTTTATGCTTTTATTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTATTTT 60
Db 225 AACGTTTATGCTTTTATTTATTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTATTTT 284

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QY 61 ATTTATTTTGT 73
Db 285 ATTTATTTGTTT 297

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RESULT 7
US-09-614-124B-571
; Sequence 571, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-571

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Query Match          97.8%; Score 71.4; DB 4; Length 402;
Best Local Similarity 98.6%; Pred. No. 3.4e-08;
Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 AACGTTTATGCTTTTATTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTATTTT 60
Db 225 AACGTTTATGCTTTTATTTATTTATTTATTTATTTATTAAGATGATTCGAGATTTATTTATTTT 284

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```

QY 61 ATTTATTTTGT 73
Db 285 ATTTATTTGTTT 297

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RESULT 8
US-09-614-124B-579
; Sequence 579, Application US/09614124B
; Patent No. 6630574
; GENERAL INFORMATION:
; APPLICANT: Wang, Tonglong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C9
; CURRENT APPLICATION NUMBER: US/09/614,124B
; CURRENT FILING DATE: 2001-07-11
; NUMBER OF SEQ ID NOS: 1668
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 579
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-614-124B-579

```

```

Query Match          97.8%; Score 71.4; DB 4; Length 402;
Best Local Similarity 98.6%; Pred. No. 3.4e-08;
Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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QY 1 AAGCTTTATATGCTTTTAAATTATTTATTTAAAGATCTCAGATATTTATTTTT 60
Db 225 AAGCTTTATATGCTTTTAAATTATTTATTTAAAGATCTCAGATATTTATTTTT 280
QY 61 ATTTPATTTTTT 73
Db 285 ATTTPATTTGTTT 297

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RESULT 9
US-09-671-325-571
; Sequence 571, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaifanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.478C12
CURRENT APPLICATION NUMBER: US/09/671.325
CURRENT FILING DATE: 2000-09-26
NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 571
; LENGTH: 402
; TYPE: DNA
; ORGANISM: Homo sapien
; US-09-671-325-571

```

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OY      1 AACGTTTATATGCTTTAAATTTAAATTTAAATTTAAAGATGATTCGAGATATTTATATTTT 60
Db      225 AACGTTTATATGCTTTATGTTTTAAATTTAAATTTAAATTTAAAGATGATTCGAGATATTTATATTTT 2844
OY      61 ATTTTATATTTTTT 73
Db      285 ATTTTATTTGTTT 297

RESULT 10
US-09-671-325-579
; Sequence 579, Application US/09671325
; Patent No. 6667154
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darrick
; APPLICANT: Rector, Marc
; APPLICANT: Mannion, Jane
; APPLICANT: Fan, Liqun
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.478C12
; CURRENT APPLICATION NUMBER: US/09/671,325
; CURRENT FILING DATE: 2000-09-26
; NUMBER OF SEQ ID NOS: 1825
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 579
; LENGTH: 402

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;      TYPE: DNA
;      ORGANISM: Homo sapien
US-09-671-325-579

Query Match      97.8%; Score 71.4; DB 4; Length 402;
Best Local Similarity 98.6%; Pred. No. 3.4e-08;
Matches 72; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY      1 AACGTTTATTGTCGTTTTTAATTATTATTAAAGATGGATTCCTCAGATATTATATTTT 60
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Db       225 AACGTTTATTGTCGTTTTTAATTATTATTAAAGATGGATTCCTCAGATATTATATTTT 284

QY      61 ATTTATTTT 73
         |||||
Db       285 ATTTATTTGTTT 297

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Oy      1 AACGTTTATGTGTTTATTTTAAATTTATTTATTAAGATGCAATTCAGATAATTTATATTTT 60
Db      225 AACGTTTATGTGTTTATTTTAAATTTATTTTAAAGATGCAATTCAGATAATTTATATTTT 284

Oy      61 ATTTTATTTT 73
      |||||
      |||||
      |||||
      |||||
Db      285 ATTTTATTTGTTT 297

RESULT 12
US-09-589-184-579
; Sequence 579, Application US/09589184
; Patent No. 6686447
; GENERAL INFORMATION:
; APPLICANT: Bangur, Tongtong
; APPLICANT: Lodes, Michael A.
; APPLICANT: Fanger, Gary
; APPLICANT: Vedvick, Tom
; APPLICANT: Carter, Darlick
; APPLICANT: Retter, Marc
; APPLICANT: Mannion, Jane
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.878C8
; CURRENT APPLICATION NUMBER: US/09/589,184

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	Matches	51;	Conservative	0;	Mismatches	22;	Indels	0;	Gaps	0;
Oy	1	AACGTTTATGCTGTTTAAATTATTTATTTAAGATGATCTCAGATTTTATTTT								60
Db	1758	AAATTTAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTTAAATTTT								1817
Oy	61	ATTTATTTT								73
Db	1818	TTTTTAAATTT								1830

Search completed: October 14, 2004, 18:42:43
 Job time : 69 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: October 14, 2004, 18:09:36 ; Search time 341 Seconds
(without alignments)

1085.274 Million cell updates/sec

Title: US-10-658-093-19

Perfect score: 73
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Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 3340653 seqs, 2534783454 residues

Total number of hits satisfying chosen parameters: 6681306

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published Applications NA:*

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13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
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16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	73	100.0	73	17	US-10-658-093-19
2	73	100.0	75	17	US-10-658-093-14
3	73	100.0	237	15	US-10-085-783A-34451
4	73	100.0	237	16	US-10-242-535A-34451
5	73	100.0	239	9	US-09-878-178-1169
6	73	100.0	239	14	US-10-046-935-1169
7	73	100.0	239	15	US-10-146-502-1169
8	73	100.0	240	13	US-10-085-783A-30739
9	73	100.0	240	16	US-10-242-535A-30739
10	73	100.0	245	13	US-10-007-926A-405
11	73	100.0	255	13	US-10-085-783A-893
12	73	100.0	255	16	US-10-242-535A-893
13	73	100.0	265	13	US-10-085-783A-19213
14	73	100.0	265	16	US-10-242-535A-19213

15	73	100.0	281	13	US-10-085-783A-26860	Sequence 26860, A
16	73	100.0	281	16	US-10-242-535A-26860	Sequence 26860, A
17	73	100.0	360	13	US-10-085-783A-29586	Sequence 29586, A
18	73	100.0	360	16	US-10-242-535A-29586	Sequence 29586, A
19	73	100.0	465	10	US-09-918-995-10176	Sequence 10176, A
20	73	100.0	477	15	US-10-101-510-243	Sequence 197, App
21	73	100.0	477	17	US-10-283-975A-197	Sequence 197, App
22	73	100.0	1163	14	US-10-002-600-39	Sequence 2057, App
23	73	100.0	1613	16	US-10-062-674-2057	Sequence 2057, App
24	73	100.0	1946	9	US-09-864-761-3420	Sequence 3420, App
25	73	100.0	2084	15	US-10-007-926A-318	Sequence 318, App
26	73	100.0	2084	16	US-10-341-434-173	Sequence 173, App
27	73	100.0	2135	10	US-09-971-392-8	Sequence 8, App1
28	73	100.0	2154	13	US-10-116-802-292	Sequence 292, App
29	73	100.0	2180	16	US-10-264-049-347	Sequence 347, App
30	73	100.0	2227	14	US-10-002-600-36	Sequence 36, App1
31	73	100.0	2461	9	US-09-925-299-129	Sequence 129, App
32	73	100.0	2461	10	US-09-925-299-129	Sequence 129, App
33	73	100.0	2461	15	US-10-106-698-289	Sequence 289, App
34	73	100.0	3565	10	US-09-960-706-993	Sequence 993, App
35	73	100.0	3565	10	US-09-873-319-649	Sequence 649, App
36	73	100.0	3565	12	US-09-873-367C-793	Sequence 793, App
37	73	100.0	3565	13	US-09-968-007A-433	Sequence 433, App
38	73	100.0	6210	13	US-10-240-425-1272	Sequence 1272, App
39	73	100.0	6210	15	US-10-101-510-201	Sequence 201, App
40	73	100.0	6210	16	US-10-440-464-135	Sequence 135, App
41	73	100.0	6210	17	US-10-717-597-141	Sequence 141, App
42	73	100.0	6210	17	US-10-775-169-188	Sequence 188, App
43	73	100.0	22477	13	US-10-087-192-1554	Sequence 1594, App
44	73	97.8	402	9	US-09-736-457-571	Sequence 571, App
45	71.4	97.8	402	9	US-09-736-457-579	Sequence 579, App

ALIGNMENTS

RESULT 1
US-10-658-093-19
Sequence 19, Application US/10658093
Publication No. US20040115704A1
GENERAL INFORMATION:
APPLICANT: Daly, John Michael
TITLE OF INVENTION: Constructs for Gene Expression Analysis
FILE REFERENCE: 12177722
CURRENT APPLICATION NUMBER: US/10/658,093
CURRENT FILING DATE: 2003-09-09
PRIOR APPLICATION NUMBER: USSN 60/274770
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: PCT/AU02/00351
PRIOR FILING DATE: 2001-03-08
NUMBER OF SEQ ID NOS: 57
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19
LENGTH: 73
TYPE: DNA
ORGANISM: mammalian
US-10-658-093-19

Query Match 100.0%; Score 73; DB 17; Length 73;
Best Local Similarity 100.0%; Pred. No. 1.1e-06;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTAAATTATTTATAGATGATTCACATATTTATTTT 60
1 AACGTTTATGCTTTTAAATTATTTATAGATGATTCACATATTTATTTT 60
Db 1 AACGTTTATGCTTTTAAATTATTTATAGATGATTCACATATTTATTTT 60
QY 61 ATTATATTTT 73
61 ATTATATTTT 73
Db 61 ATTATATTTT 73

RESULT 2
US-10-658-093-14

Db 130 ATTTATTTTTTT 118

RESULT 6

US-10-046-935-1169/C
Sequence 1169, Application US/10046935
Publication No. US20020156011A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aijun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.527C1
CURRENT APPLICATION NUMBER: US/10/046,935
CURRENT FILING DATE: 2002-01-15
NUMBER OF SEQ ID NOS: 2239
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1169
LENGTH: 239
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 223
OTHER INFORMATION: n = A,T,C or G
US-10-046-935-1169

Query Match 100.0%; Score 73; DB 14; Length 239;
Best Local Similarity 100.0%; Pred. No. 1,4e-06;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTAAATTATTAATTAAGATGATCTCAGATATTATTTT 60

Db 190 AACGTTTATGCTTTTAAATTATTAATTAAGATGATCTCAGATATTATTTT 131

QY 61 ATTTATTTTTTT 73

Db 130 ATTTATTTTTTT 118

RESULT 7

US-10-146-502-1169/C
Sequence 1169, Application US/10146502
Publication No. US20030069180A1
GENERAL INFORMATION:
APPLICANT: Jiang, Yugu
APPLICANT: Harlocker, Susan L.
APPLICANT: Secrist, Heather
APPLICANT: Wang, Aijun
APPLICANT: Stolk, John A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
FILE REFERENCE: 210121.527C2
CURRENT APPLICATION NUMBER: US/10/146,502
CURRENT FILING DATE: 2002-05-14
NUMBER OF SEQ ID NOS: 2241
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1169
LENGTH: 239
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: 223
OTHER INFORMATION: n = A,T,C or G
US-10-146-502-1169

Query Match 100.0%; Score 73; DB 15; Length 239;
Best Local Similarity 100.0%; Pred. No. 1,4e-06;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTAAATTATTAATTAAGATGATCTCAGATATTATTTT 60

Db 190 AACGTTTATGCTTTTAAATTATTAATTAAGATGATCTCAGATATTATTTT 131

QY 61 ATTTATTTTTTT 73

Db 130 ATTTATTTTTTT 118

RESULT 8

US-10-085-783A-30739
Sequence 30739, Application US/10085783A
Publication No. US20040037841A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002
CURRENT APPLICATION NUMBER: US/10/085,783A
CURRENT FILING DATE: 2002-02-28
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 30739
LENGTH: 240
TYPE: DNA
ORGANISM: Human
US-10-085-783A-30739

Query Match 100.0%; Score 73; DB 13; Length 240;
Best Local Similarity 100.0%; Pred. No. 1,4e-06;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTTTTAAATTATTAATTAAGATGATCTCAGATATTATTTT 60

Db 62 AACGTTTATGCTTTTAAATTATTAATTAAGATGATCTCAGATATTATTTT 121

QY 61 ATTTATTTTTTT 73

Db 122 ATTTATTTTTTT 134

RESULT 9

US-10-242-535A-30739
Sequence 30739, Application US/10242535A
Publication No. US20040013663A1
GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.
APPLICANT: Liew, C.C.
TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005
CURRENT APPLICATION NUMBER: US/10/242,535A
CURRENT FILING DATE: 2002-09-12
PRIOR FILING DATE: 2002-02-28
PRIOR APPLICATION NUMBER: US 60/305,340
PRIOR FILING DATE: 2001-07-13
PRIOR APPLICATION NUMBER: US 60/275,017
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: US 60/271,955
PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 30739
LENGTH: 240
TYPE: DNA
ORGANISM: Human

US-10-242-535A-30739

Query Match

Best Local Similarity 100.0%; Score 73; DB 16; Length 240;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTTTAAAGATGATCTCAGATATTATTTT 60
 DB 62 AACGTTTATGCTGTTTAAATTTTAAAGATGATCTCAGATATTATTTT 121
 QY 61 ATTTATTTTTTT 73
 DB 122 ATTTATTTTTTT 134

RESULT 10

US-10-007-926A-405/c

Sequence 405, Application US/10007926A
 Publication No. US20030143539A1

GENERAL INFORMATION:
 APPLICANT: BERTUCCI, FRANCOIS
 APPLICANT: HOUIGATTE, REMI
 APPLICANT: BIRBAUD, DANIEL
 APPLICANT: NGUYEN, CATHERINE
 APPLICANT: VIENS, PATRICE
 APPLICANT: PERT, VINCENT
 TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
 TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
 FILE REFERENCE: 1546-R-00
 CURRENT APPLICATION NUMBER: US/10/007,926A
 CURRENT FILING DATE: 2001-12-07
 PRIOR APPLICATION NUMBER: 60/254,090
 PRIOR FILING DATE: 2000-12-08
 NUMBER OF SEQ ID NOS: 468
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 405
 LENGTH: 245
 TYPE: DNA
 ORGANISM: Homo sapiens

FEATURE:
 OTHER INFORMATION: 5' terminal sequence. v-fos fdj murine
 OTHER INFORMATION: osteosarcoma viral oncogene homolog (FOS) gene.

FEATURE:
 NAME/KEY: modified_base
 LOCATION: (204)
 OTHER INFORMATION: a, t, c or g
 FEATURE:
 NAME/KEY: modified_base
 LOCATION: (223)
 OTHER INFORMATION: a, t, c or g
 FEATURE:
 NAME/KEY: modified_base
 LOCATION: (230)
 OTHER INFORMATION: a, t, c or g
 FEATURE:
 NAME/KEY: modified_base
 LOCATION: (237)
 OTHER INFORMATION: a, t, c or g
 FEATURE:
 NAME/KEY: modified_base
 LOCATION: (240)
 OTHER INFORMATION: a, t, c or g
 FEATURE:
 NAME/KEY: modified_base
 LOCATION: (242)
 OTHER INFORMATION: a, t, c or g
 ;
 US-10-007-926A-405

Query Match 100.0%; Score 73; DB 15; Length 245;

Best Local Similarity 100.0%; Pred. No. 1,4e-06;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTTTAAAGATGATCTCAGATATTATTTT 60
 DB 180 AACGTTTATGCTGTTTAAATTTTAAAGATGATCTCAGATATTATTTT 121
 QY 61 ATTTATTTTTTT 73
 DB 120 ATTTATTTTTTT 108

RESULT 11

US-10-085-783A-893

Sequence 893, Application US/10085783A
 Publication No. US20040037841A1

GENERAL INFORMATION:
 APPLICANT: ChondroGene Inc.
 APPLICANT: Liew, C.C.
 TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 FILE REFERENCE: 4231/2002
 CURRENT APPLICATION NUMBER: US/10/085,783A
 CURRENT FILING DATE: 2002-02-28
 PRIOR APPLICATION NUMBER: US 60/305,340
 PRIOR FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US 60/275,017
 PRIOR FILING DATE: 2001-03-12
 PRIOR APPLICATION NUMBER: US 60/271,955
 PRIOR FILING DATE: 2001-02-28
 NUMBER OF SEQ ID NOS: 58994
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 893
 LENGTH: 255
 TYPE: DNA
 ORGANISM: Human
 US-10-085-783A-893

Query Match 100.0%; Score 73; DB 13; Length 255;
 Best Local Similarity 100.0%; Pred. No. 1,4e-06;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTTTAAAGATGATCTCAGATATTATTTT 60
 DB 67 AACGTTTATGCTGTTTAAATTTTAAAGATGATCTCAGATATTATTTT 126
 QY 61 ATTTATTTTTTT 73
 DB 127 ATTTATTTTTTT 139

RESULT 12

US-10-242-535A-893

Sequence 893, Application US/10242535A
 Publication No. US20040013663A1

GENERAL INFORMATION:
 APPLICANT: ChondroGene Inc.
 APPLICANT: Liew, C.C.
 TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
 FILE REFERENCE: 4231/2005
 CURRENT APPLICATION NUMBER: US/10/242,535A
 CURRENT FILING DATE: 2002-09-12
 PRIOR APPLICATION NUMBER: US 10/085,783
 PRIOR FILING DATE: 2002-02-28
 PRIOR APPLICATION NUMBER: US 60/305,340
 PRIOR FILING DATE: 2001-07-13
 PRIOR APPLICATION NUMBER: US 60/275,017
 PRIOR FILING DATE: 2001-03-12
 PRIOR APPLICATION NUMBER: US 60/271,955
 PRIOR FILING DATE: 2001-02-28
 NUMBER OF SEQ ID NOS: 58994
 SOFTWARE: PatentIn version 3.2
 SEQ ID NO 893
 LENGTH: 255

TYPE: DNA
ORGANISM: Human
US-10-242-535A-893

Query Match 100.0%; Score 73; DB 16; Length 255;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTATTAATGAATGATTCCTCAGATTTATATTTT 60
DB 67 AACGTTTATGCTGTTTAAATTATTAATGAATGATTCCTCAGATTTATATTTT 126
QY 61 ATTTATTTTTTT 73
DB 127 ATTTATTTTTTT 139

RESULT 13

US-10-085-783A-19213
Sequence 19213, Application US/10085783A
Publication No. US20040037841A1

GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085, 783A

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PatentIn version 3.2

SEQ ID NO 19213

LENGTH: 265

TYPE: DNA

ORGANISM: Human

US-10-085-783A-19213

Query Match 100.0%; Score 73; DB 13; Length 265;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTATTAATGAATGATTCCTCAGATTTATATTTT 60
DB 85 AACGTTTATGCTGTTTAAATTATTAATGAATGATTCCTCAGATTTATATTTT 144
QY 61 ATTTATTTTTTT 73
DB 145 ATTTATTTTTTT 157

RESULT 14

US-10-242-535A-19213
Sequence 19213, Application US/10242535A
Publication No. US20040013663A1

GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2005

CURRENT APPLICATION NUMBER: US/10/242, 535A

CURRENT FILING DATE: 2002-09-12

PRIOR APPLICATION NUMBER: US 10/085, 783

PRIOR FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR FILING DATE: 2001-02-28
NUMBER OF SEQ ID NOS: 58994
SOFTWARE: PatentIn version 3.2
SEQ ID NO 19213

Query Match 100.0%; Score 73; DB 16; Length 265;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTATTAATGAATGATTCCTCAGATTTATATTTT 60
DB 85 AACGTTTATGCTGTTTAAATTATTAATGAATGATTCCTCAGATTTATATTTT 144
QY 61 ATTTATTTTTTT 73
DB 145 ATTTATTTTTTT 157

RESULT 15

US-10-085-783A-26860
Sequence 26860, Application US/10085783A
Publication No. US20040037841A1

GENERAL INFORMATION:
APPLICANT: ChondroGene Inc.

TITLE OF INVENTION: Compositions and Methods Relating to Osteoarthritis
FILE REFERENCE: 4231/2002

CURRENT APPLICATION NUMBER: US/10/085, 783A

CURRENT FILING DATE: 2002-02-28

PRIOR APPLICATION NUMBER: US 60/305,340

PRIOR FILING DATE: 2001-07-13

PRIOR APPLICATION NUMBER: US 60/275,017

PRIOR FILING DATE: 2001-03-12

PRIOR APPLICATION NUMBER: US 60/271,955

PRIOR FILING DATE: 2001-02-28

NUMBER OF SEQ ID NOS: 58994

SOFTWARE: PatentIn version 3.2

SEQ ID NO 26860

LENGTH: 281

TYPE: DNA

ORGANISM: Human

US-10-085-783A-26860

Query Match 100.0%; Score 73; DB 13; Length 281;
Best Local Similarity 100.0%; Pred. No. 1.4e-06;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTATTAATGAATGATTCCTCAGATTTATATTTT 60
DB 102 AACGTTTATGCTGTTTAAATTATTAATGAATGATTCCTCAGATTTATATTTT 161
QY 61 ATTTATTTTTTT 73
DB 162 ATTTATTTTTTT 174

Search completed: October 14, 2004, 19:34:13
Job time : 343 secs

Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/ICR Human Cancer Genome Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/scripts/gethtml2.pl?l=et2-RC4-ET0024-2300500-013-et0&t3=2000-05-29&t4=1>)
Seq primer: puc 18 forward
High quality sequence start: 16
High quality sequence stop: 183.
Inserts/Deletions

FEATURES

SOURCE

```

1..183
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="ET0024"
/note="Organ: lung tumor; Vector: puc18, Site.1: SmaI;
Site.2: SmaI; A mini-library was made by cloning products
derived from ORSTS PCR (U.S. Letters Patent application
No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

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ORIGIN

Query Match	100.0%	Score 73;	DE 10;	Length 183;
Similarity	100.0%	Pred. No. 0.007;		
Best Local				
Matches 73;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;

DY 1 AACGTTTATGTGTTTTAATTATTTATTAAGATGGATCTCAGATAATTATATTTT 60

DB 97 AACGTTTATGTGTTTTAATTATTTATTAAGATGGATTCAGATAATTATATTTT 38

QY	61	ATTTTATTTT	73
Db	37	ATTTTATTTT	25

RESULT 2

LOCUS	CA842273	214 bp	mRNA	linear	EST 13-DEC-2002
DEFINITION	ig93f12.x1 HR85 islet Homo sapiens cDNA clone IMAGE: 3', mRNA sequence.				

ACCESSION	CA842273
VERSION	CA842273.1
KEYWORDS	EST.
SOURCE	Homo sapiens (human)

REFERENCE
AUTHORS
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K.,
Mammalia, Eutheria, Primates, Carnarhini, Homiidae, Homo.
1 (bases 1 to 214)

Hillier, L., Marra, M., Pape, D., Wylie, T., Martin, J., Blistein, A., Schmitz, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCan, R., Cole, R., Tsagariseli, R., Williams, T., Jackson, Y., and Bowers, Y.

TITLE	JOURNAL	COMMENT
Endocrine Pancreas Consortium Unpublished (2000)		Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138
Tel: 617-495-1812

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)

FEATURES
Seq primer: -40UP from Gibco
High quality sequence stop: 203.
Location/Qualifiers

FEATURES
SOURCE

```

/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:"
/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/clone_idb="HR85 islet"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site:1;
NotI; Site 2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size ~1kb. 5'
XhoI site was destroyed after directional cloning.
Amplified once. Contact Information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permut Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@igate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

```

ORIGIN

Query Match	100.0%;	Score 73;	DB 14;	Length 214;
Best Local Similarity	100.0%;	Pred. No. 0.0064;		
Matches 73; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

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Oy      1 AACGTTTAAATGTGGTTTTAATTATTAATTAAGATCGATTCAGATAATTATATTTT    60
        |||||
Db     197 AACGTTTAAATGTGGTTTTAATTATTAATTAAGATCGATTCAGATAATTATATTTT    13
```

QY	61	ATTTTTATTTTTTTT	73
Db	137	ATTTTATTTTTTTT	129

RESULT 3

LOCUS DEFINITION	216 bp	mRNA	linear	EST 28-AUG-1995
DD8202				
HUM355D05B	Clontech human aorta polyA+	mRNA (#6572)		
CDNA clone GEN-355D05 5'	mRNA sequence.			
				Homo sapiens

VERSION	D58202.1	GI:964824
KEYWORDS	EST.	
SOURCE	Homo sapiens (human)	

REFERENCE

1 (bases 1 to 216)

BUKARYOTA; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

FUJIWARA, T., HIRANO, H., KATAGIRI, T., KAWAI, A., KUGA, Y., NAGATA, M.,

AUTHORS

TITLES
Okuno, S., Ozaki, K., Shimizu, F., Shimoda, Y., Shinomiya, H.,
Takaichi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y.,
Maekawa, H., Shin, S. and Nakamura, Y.
Fujiwara et al. (1995)

COMMENT
Contact: Tsutomu Fujiwara
Otsuka GEN Research Institute
Otsuka Pharmaceutical Co., Ltd
463-10 Kagasuno Kawanishi-cho, Tokushima, Tokushima, 771-01 Japan

FEATURES
source
Fax: 0886-37-1035.
Location/Qualifiers
1. .216
Location-#None

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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="GEN-355D05"
/clone_1b="Clontech human aorta polyA+ mRNA (#6572)"

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ORIGIN

Query Match	100.0%	Score 73;	DB 14;	Length 216;
Best Local Similarity	100.0%	Pred. No. 0.0063;		
Matches 73; Conservative	0;	Mismatches 0;	Indels 0;	Gaps 0;

QY	1	AACGTTTATGCTGTTTAAATTATTTATTAAGATGCTCAGATTTATATTTT	60
DB	35	AACGTTTATGCTGTTTAAATTATTTATTAAGATGCTCAGATTTATATTTT	94
QY	61	ATTTTATTTT	73
DB	95	ATTTTATTTT	107
RESULT 4			
LOCUS	R79209/c		
DEFINITION	R79209	243 bp	mRNA
ACCESSION	Y188b05.g1	Soares placenta NB2HP	Homio sapiens cDNA clone
VERSION	IMAGE:146289.3	similar to gb:V01512_mna5	P55-C-FOS PROTO-ONCOGENE
KEYWORDS	PROTEIN (HUMAN);	mRNA sequence.	
SOURCE	R79209		
ORGANISM	R79209.1	GI:855490	
	EST.		
	Homio sapiens	(human)	
	Buazayota; Metazoa;	Chordata; Craniata;	Vertebrate; Euteleostomi;
	Mammalia; Eutheria;	Primates; Cactarrhini;	Homnidae; Homo.
REFERENCE	1	(bases 1 to 243)	
AUTHORS	Hillier, L., Clark, N., Dubuque, T., Ellstrom, K., Hawkins, M., Holman, M., Holtman, M., Kucaba, T., Le, M., Lennon, G., Marra, M., Parsons, J., Rifkin, B., Rohlfing, T., Soares, M., Tan, P., Tsvetakis, E., Waterston, R., Williamson, A., Wohldmann, P. and Wilson, R.		
TITLE	The Mashu-Merck EST Project		
JOURNAL	Unpublished (1995)		
COMMENT	Contact: Wilson RK		
	Washington University School of Medicine		
	444 Forest Park Parkway, Box 8501, St. Louis, MO 63108		
	Tel: 314 286 1800		
	Fax: 314 286 1810		
	Email: eest@watson.wustl.edu		
	Insert Size: 800		
	High quality sequence stops: 241		
	Source: IMAGE Consortium, LNL		
	This clone is available royalty-free through LNL; contact the		
	IMAGE Consortium (info@image.lnl.gov) for further information.		
	Insert Length: 800	Std Error: 0.00	
	Seq primer: Promega -21ml3		
	High quality sequence stop: 241.		
FEATURES	Location/Qualifiers		
source	1..243		
	/organism="Homio sapiens"		
	/mol_type="mRNA"		
	/db_xref="GDB:557815"		
	/db_xref="taxon:9606"		
	/clone="IMAGE:146289"		
	/sex="Female"		
	/dev_stage="placenta obtained at birth (full term)"		
	/lab_host="DH10B (ampicillin resistant)"		
	/clone_lib="Soares placenta NB2HP"		
	/note="Organ: Placenta; Vector: pT73D (Pharmacia) with a		
	modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st		
	strand cDNA was primed with a Not I - oligo(dT) primer [5'		
	AACGGAAGAATTCGCGCGCAGAGAAATTTTATTTTATTTT 3']		
	double-stranded cDNA was ligated to Eco RI adaptors		
	(Pharmacia), digested with Not I and cloned into the Not I		
	and Eco RI sites of the modified pT73 vector. Library		
	went through one round of normalization. Library		
	constructed by Bento Soares and M. Fatima Bonaldo.		
ORIGIN			
Query Match	100.0%	Score 73;	DB 14; Length 243;
Best Local Similarity	100.0%;	Pred. No. 0.0059;	
Matches	73;	Conservative 0;	Mismatches 0; Indels 0; Gaps 0;
QY	1	AACGTTTATGCTGTTTAAATTATTTATTAAGATGCTCAGATTTATATTTT	60
DB	155	AACGTTTATGCTGTTTAAATTATTTATTAAGATGCTCAGATTTATATTTT	96

RESULT 5	AA020879/c	245 bp	mRNA	linear	EST 30-JAN-1997
LOCUS	AA020879/c				
DEFINITION	z64693.1 r1 Soares retina N2b4HR Homo sapiens CDNA clone				
	IMAGE3:363796 5', similar to gb:V01512_rnas P55-C-FOS PROTO-ONCOGENE				
	PROTEIN (HUMAN), , mRNA sequence.				
ACCESSION	AA020879				
VERSION	AA020879.1				
KEYWORDS	EST.				
SOURCE	AA020879.1 GI:1484650				
ORGANISM	Homo sapiens (human)				
REFERENCE	Homo sapiens				
AUTHORS	Eukaryote; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 245) Hillier, S., Dietrich, N., Dubuque, T., Favetto, A., Gish, W., Chisose, S., Dietrich, N., Dubuque, T., Favetto, A., Gish, W., Hawkins, M., Hultman, M., Kucaba, T., Lacy, M., Le, M., Le, N., Mardis, E., Moore, B., Morris, M., Parsons, J., Prange, C., Rifkin, L., Rohlfing, T., Schellenberg, K., Soares, M. B., Tan, F., Thierly-Meg, J., Trevaakis, E., Underwood, K., Wohldmann, P., Waterston, R., Wilson, R. and Marra, M.				
TITLE	Generation and analysis of 280,000 human expressed sequence tags				
JOURNAL	Genome Res. 6 (9), 807-828 (1996)				
MEDLINE	97044478				
PUBMED	8889549				
COMMENT	Contact: Wilson RK Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: east@wustl.wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.lnl.gov) for further information. Insert Length: 2316 Std Error: 0.00 Seq primer: -28M13 rev2 from Amersham High quality sequence stop: 155. Location/Qualifiers 1. 245 /organism="Homo sapiens" /mol_type="mRNA" /db_xref="GDB:1280499" /db_xref="taxon:9606" /clone="IMAGE:363796" /sex="male" /tissue_type="retina" /dev_stage="55 year old" /lab_host="DH10B (ampicillin resistant)" /clone_idb="Soares retina N2b4HR" /note="Organ: eye; Vector: pRTT3 (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5' TGTTCACATCTGAGGTGGAGCGCGCCCTTTTCTTTTCTTTT 3'], double-stranded cDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pRTT3 vector (Pharmacia). The retinas were obtained from a 55 year old Caucasian and total cellular poly(a)+ RNA was extracted 6 hrs after their removal. The retina RNA was kindly provided by Roderick R. McInnes M.D. Ph.D. From the University of Toronto. Library constructed by Bento Soares and M.Facima Bernaldo."				
ORIGIN					
Query Match	100.0%;	Score 73;	DB 9;	Length 245;	
Best Local Similarity	100.0%;	Fed. No. 0.0056;			
Matches 73;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	

QY 1 AACGTTTATGCTGTTTAAATTATTAATTAAGATGATCTCAGATATTAATTTT 60
 |||||
 DB 180 AACGTTTATGCTGTTTAAATTATTAATTAAGATGATCTCAGATATTAATTTT 121
 |||||
 QY 61 ATTTATTTT 73
 |||||
 DB 120 ATTTATTTT 108
 |||||

RESULT 6
 D57391 284 bp mRNA linear EST 28-AUG-1995
 LOCUS HNM299H07A Clontech human aorta polyA+ mRNA (#6572) Homo sapiens
 DEFINITION CDNA clone GEN-299H07 3', mRNA sequence.
 VERSION D57391
 KEYWORDS D57391.1 GI:964013
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 284)
 Fujisawa, T., Hirano, H., Katagiri, T., Kawai, A., Kuga, Y., Nagata, N.,
 Okuno, S., Ozaki, K., Shimizu, F., Shimada, Y., Shinomiya, H.,
 Takachi, A., Takeda, S., Watanabe, T., Takahashi, E., Hirai, Y.,
 Maekawa, H., Shin, S. and Nakamura, Y.
 Fujisawa et al. (1995)
 TITLE Unpublished (1995)
 JOURNAL Contact: Tautomu Fujisawa
 COMMENT Otsuka GEN Research Institute
 Otsuka Pharmaceutical Co., Ltd
 463-10 Kagasuno Kawachi-cho, Tokushima, Tokushima, 771-01 Japan
 Tel: 0886-65-2888
 Fax: 0886-37-1035.

FEATURES
 source
 1..284
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="GEN-299H07"
 /clone_1ib="Clontech human aorta polyA+ mRNA (#6572)"
 Location/Qualifiers

ORIGIN
 Query Match 100.0%; Score 73; DB 14; Length 284;
 Best Local Similarity 100.0%; Pred. No. 0.0053;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTATTAATTAAGATGATCTCAGATATTAATTTT 60
 |||||
 DB 182 AACGTTTATGCTGTTTAAATTATTAATTAAGATGATCTCAGATATTAATTTT 123
 |||||
 QY 61 ATTTATTTT 73
 |||||
 DB 122 ATTTATTTT 110
 |||||

RESULT 7
 BM955729 291 bp mRNA linear EST 30-SEP-2002
 LOCUS EST0664 HEV PCR-select Homo sapiens CDNA clone HEV1046 similar to
 DEFINITION protooncogene c-fos, mRNA sequence.
 VERSION BM955729
 KEYWORDS BM955729.1 GI:23345960
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 291)
 Palmeri, D., Zhou, F.-R., Rosen, S.D. and Hemmerich, S.
 Gene expression profiling of peripheral lymph node addressin+ high
 endothelial venule cells from human tonsil: implications in
 lymphocyte recirculation and inflammation

JOURNAL Unpublished (2002)
 COMMENT Contract: Rosen SD
 Department of Anatomy
 University of California at San Francisco
 HSW-1320, 513 Parnassus Ave., San Francisco, CA 94143-0452, USA
 Tel: 415 476 1579
 Fax: 415 476 4845
 Email: sd@itsa.ucsf.edu
 Seq primer: M13 reverse.
 Location/Qualifiers
 1..291
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="HEV#1046"
 /cell_type="high endothelial"
 /clone_1ib="HEV PCR-select"
 /note="Organ: tonsil; Vector: PCR1; Site 1: EcoRI;
 Site 2: EcoRI; High endothelial cells (HEC) were isolated
 from human tonsils using magnetic beads derivatized with
 MECA-79 antibody specific to the peripheral lymph node
 addressin. CDNA was prepared from these cells using
 Cap-finder methodology, then cDNA prepared from tonsillar
 lymphocytes and from human umbilical vein endothelial
 cells were subtracted from the HEC cDNA, followed by
 normalization through selective PCR amplification."

ORIGIN
 Query Match 100.0%; Score 73; DB 12; Length 291;
 Best Local Similarity 100.0%; Pred. No. 0.0052;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTAAATTATTAATTAAGATGATCTCAGATATTAATTTT 60
 |||||
 DB 97 AACGTTTATGCTGTTTAAATTATTAATTAAGATGATCTCAGATATTAATTTT 156
 |||||
 QY 61 ATTTATTTT 73
 |||||
 DB 157 ATTTATTTT 169
 |||||

RESULT 8
 BF436565/c 331 bp mRNA linear EST 29-NOV-2000
 LOCUS 7p15f03.x1 NCI CGAP Br22 Homo sapiens CDNA clone IWAGS:3645845 3',
 DEFINITION mRNA sequence.
 VERSION BF436565
 KEYWORDS BF436565.1 GI:11448880
 SOURCE EST.
 ORGANISM Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 REFERENCE 1 (bases 1 to 331)
 NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 Tumor Gene Index
 Unpublished (1997)
 JOURNAL Contact: Robert Strusberg, Ph.D.
 Email: cgs@bcr-romail.nih.gov
 Tissue Procurement: Chris Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.
 CDNA Library Preparation: Life Technologies, Inc.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the I.M.A.G.E. Consortium/ILNI, send email to:
 info@image.llnl.gov
 Seq primer: -40UP from Gibco
 High quality sequence stop: 308.
 Location/Qualifiers
 1..331
 /organism="Homo sapiens"

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_image="3645845"
/tissue_type="invasive ductal carcinoma, 3 pooled samples"
/lab_host="DH10B (TI-phase resistant)"
/clone_lib="NCI CGAP Br22"
/note="Organ: breast; Vector: PCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.5 Kb. Constructed by Life
Technologies."

ORIGIN

Query Match 100.0%; Score 73; DB 10; Length 331;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTATTTATTTATTAAGATGATTCGATATTTATTTT 60
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DB 187 AACGTTTATGCTGTTTATTTATTTATTTATTAAGATGATTCGATATTTATTTT 128

QY 61 ATTTATTTT 73
|||
DB 127 ATTTATTTT 115

RESULT 9
BP752720/c 334 bp mRNA linear EST 10-JAN-2001

LOCUS RC4-BN0408-271100-013-409 BN0408 Homo sapiens cDNA, mRNA sequence.
DEFINITION BP752720
ACCESSION BP752720.1 GI:12079396

VERSION BP752720.1 GI:12079396
KEYWORDS EST.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (bases 1 to 334)
Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., da Silva,W. Jr., Zago,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Marukuma,A., Bata,G.S., Simpson,D.H.,
Bruneir,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V.,
O'Hare,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
Simpson,A.J.

COMMENT Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
Proc. Natl. Acad. Sci. U.S.A. 97 (7), 3491-3496 (2000)

TITLE
JOURNAL
MEDLINE
PUBMED

20202663
10737800
Contact: Simpson A.J.G.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?l=RC4&t2=RC4-BN0408-
271100-013-409&t3=2000-11-27&t4=1)
Seq primer: puc 18 forward
High quality sequence start: 29
High quality sequence stop: 334.
Location/Qualifiers

FEATURES

1..334
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/dev_stage="Adult"
/clone_lib="BN0408"
/note="Organ: breast; normal; Vector: puc18; Site 1: SmaI;
Site 2: SmaI; A mini-library was made by cloning products
derived from ORFESTES PCR (U.S. Letters Patent application

No. 196,716 - Ludwig Institute for Cancer Research)
profiles into the pUC 18 vector. Reverse transcription of
tissue mRNA and cDNA amplification were performed under
low stringency conditions."

ORIGIN

Query Match 100.0%; Score 73; DB 10; Length 334;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTATTTATTTATTTATTAAGATGATTCGATATTTATTTT 60
|||
DB 102 AACGTTTATGCTGTTTATTTATTTATTTATTTATTAAGATGATTCGATATTTATTTT 43

QY 61 ATTTATTTT 73
|||
DB 42 ATTTATTTT 30

RESULT 10

AM347336 337 bp mRNA linear EST 09-JUL-2000
LOCUS AM347336
DEFINITION 30736 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.
ACCESSION AM347336
VERSION AM347336.1 GI:6844983

KEYWORDS EST.
SOURCE Sus scrofa (pig)
Sus scrofa

ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.
REFERENCE 1 (bases 1 to 337)
Fahrenkrug,S.C., Smith,T.P.L., Freking,B.A., Cho,J., White,J.,
Vallet,J., Wise,T., Rohrer,G.A., Pertea,G., Sultana,R.,
Quackenbush,J. and Keefe,J.W.
Porcine gene discovery by normalized cDNA-library sequencing and
EST cluster assembly
Mamm. Genome 13 (8), 475-478 (2002)

TITLE
JOURNAL
MEDLINE
PUBMED
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 20
and -mismatch 12 options.
PCR primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCGCCGTCACGACG
Plate: 9 row: L column: 21
Seq primer: ATTTAGGTGACACTATG.
Location/Qualifiers

FEATURES

1..337
/organism="Sus scrofa"
/mol_type="mRNA"
/db_xref="taxon:9823"
/tissue_type="pooled"
/lab_host="DH10B"
/clone_lib="MARC 1Pig"
/note="Vector: PCMV SPORT6; Site 1: NotI; Site 2: SalI;
library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."

ORIGIN

Query Match 100.0%; Score 73; DB 10; Length 337;
Best Local Similarity 100.0%; Pred. No. 0.0048;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACGTTTATGCTGTTTATTTATTTATTTATTAAGATGATTCGATATTTATTTT 60
|||
DB 165 AACGTTTATGCTGTTTATTTATTTATTTATTTATTAAGATGATTCGATATTTATTTT 224

QY 61 ATTTATTTTTTTT 73
 DB 225 ATTTATTTTTTTT 237
 RESULT 11
 LOCUS CA771107/c
 DEFINITION 1070h05.x1 HR85 1slet Homo sapiens cDNA clone IMAGE:6131937 3', mRNA sequence.
 ACCESSION CA771107
 VERSION CA771107.1 GI:26008149
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 338)
 AUTHORS Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Leshchka, I., Scharce, M., Brestelli, J., Gradwohl, G., Clifton, S., Hillier, L., Marra, M., Page, D., Wylie, T., Martin, J., Bistahn, A., Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagaris, V., Williams, T., Jackson, Y., and Bowers, Y.
 COMMENT Endocrine Pancreas Consortium
 Unpublished (2000)
 CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@iobp.harvard.edu
 Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
 Seq primer: -40UP from Gibco
 High quality sequence stop: 313.
 FEATURES
 SOURCE
 1..338
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:6131937"
 /tissue_type="Purified pancreatic 1slet"
 /lab_host="DH10B"
 /clone_1lb="HR85 1slet"
 /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size-selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt Lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."
 ORIGIN
 Query Match 100.0%; Score 73; DB 14; Length 338;
 Best Local Similarity 100.0%; Pred. No. 0.0047;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AACGTTTATGCTTTTATTTATTTATTAAGATGATCTCGATATTATTTT 60
 DB 198 AACGTTTATGCTTTTATTTATTTATTAAGATGATCTCGATATTATTTT 139
 QY 61 ATTTATTTTTTTT 73
 DB 138 ATTTATTTTTTTT 126

RESULT 12
 LOCUS CA434443/c
 DEFINITION UI-H-D10-ary-h-05-0-UI.s1 NCI CGAP D10 Homo sapiens cDNA clone
 ACCESSION CA434443
 VERSION CA434443.1 GI:24798863
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 339)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
 COMMENT Unpublished (1997)
 CONTACT: Robert Straube, Ph.D.
 Email: cgap@bme.mil.nih.gov
 Tissue Procurement: Dr. Jose Mercuende
 cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa
 cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
 DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
 Clone Distribution: Clone distribution information can be obtained from Dr. M. Bento Soares, bento-soares@uiowa.edu
 The following repetitive elements were found in this cDNA sequence: 122-148, >AT rich#low_complexity (matched complement)
 Seq primer: M13 FORWARD
 POLYA=Yes.
 FEATURES
 SOURCE
 1..339
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="UI-H-D10-ary-h-05-0-UI"
 /tissue_type="Lung Focal Fibrosis"
 /dev_stage="Adult"
 /lab_host="DH10B (Life Technologies)"
 /clone_1lb="NCI CGAP D10"
 /note="Organ: Lung; Vector: pRT3-Pac (Pharmacia) with a modified polylinker; Site_1: EcoR I; Site_2: Not I; NCI CGAP D10 is a cDNA library containing the following tissue(s): A pool of Lung Focal Fibrosis. The library was constructed according to Bonaldo, Lennon and Soares, Genome Research, 6:791-806, 1996. First strand cDNA synthesis was primed with an oligo-dT primer containing a Not I site. Double stranded cDNA was ligated to an EcoR I adaptor, digested with Not I, and cloned directionally into pRT3-Pac vector. The oligonucleotide used to prime the synthesis of first-strand cDNA contains a library tag sequence that is located between the Not I site and the (drr)18 tail. The sequence tag for this library is ATACGGGTC.
 TAG_TISSUE=Lung with fibrosis
 TAG_LIB=UI-H-D10
 TAG_SEQ=ATACGGGTC"
 ORIGIN
 Query Match 100.0%; Score 73; DB 14; Length 339;
 Best Local Similarity 100.0%; Pred. No. 0.0047;
 Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 AACGTTTATGCTTTTATTTATTTATTAAGATGATCTCGATATTATTTT 60
 DB 194 AACGTTTATGCTTTTATTTATTTATTAAGATGATCTCGATATTATTTT 135
 QY 61 ATTTATTTTTTTT 73
 DB 134 ATTTATTTTTTTT 122
 RESULT 13

CB068539/c
LOCUS CB068539 350 bp mRNA linear EST 21-JAN-2003
DEFINITION 1829d11.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6553965 3', mRNA sequence.
ACCESSION CB068539
VERSION CB068539.1 GI:27813059
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 350)
Melton, D., Brown, J., Kenty, G., Permutt, A., Lee, C., Kaestner, K., Lentschka, I., Scarsce, M., Bresselli, J., Gradwohl, G., Clifton, S., Hillier, L., Warr, M., Page, D., Wylie, T., Martin, J., Bilsstein, A., Schmitt, A., Theising, B., Ritter, E., Ronko, I., Bennett, J., Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarisvalli, R., Williams, T., Jackson, Y., and Bowers, Y.
Endocrine Pancreas Consortium
Unpublished (2000)
CONTACT: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
Endocrine Pancreas Consortium
Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
Tel: 617-495-1812
Fax: 617-495-8557
Email: dmelton@iuhp.harvard.edu
Library was constructed by Dr. Hiroshi Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
Seq primer: -40RP from Glibco
High quality sequence stop: 317.
Location/Qualifiers
1. 350
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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/tissue_type="Purified pancreatic islet"
/lab_host="DH10B"
/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1: NotI; Site_2: XhoI; cDNA made by oligo-dT priming. Size selected on agarose gel. Average insert size ~1kb. 5' XhoI site was destroyed after directional cloning. Amplified once. Contact information: Hiroshi Inoue, MD, Metabolism Div. (Alan Permutt lab), Washington University School of Medicine, Box 8127, 660 South Euclid Ave., St. Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel: 314-362-1916, Fax: 314-747-2692."

ORIGIN
Query Match 100.0%; Score 73; DB 14; Length 350;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGTTTATGTTGTTTAAATTATTTATTAAGATGATTCAGATATTATATTTT 60
DB 195 AACGTTTATGTTGTTTAAATTATTTATTAAGATGATTCAGATATTATATTTT 136
QY 61 ATTTATTTTTTT 73
DB 135 ATTTATTTTTTT 123

RESULT 14
LOCUS AM021706 351 bp mRNA linear EST 13-SEP-1999
DEFINITION d527p10.y1 Morton Fetal Cochlea Homo sapiens cDNA clone
IMAGE:2484450 5', mRNA sequence.
ACCESSION AM021706

VERSION AM021706.1 GI:5875236
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 351)
Robertson, N.G., Khetarpal, U., Gutierrez-Espeleta, G.A., Bieber, F.R., and Morton, C.C.
Isolation of novel and known genes from a human fetal cochlear cDNA library using subtractive hybridization and differential screening
Genomics 23, 42-50 (1994)
7829101
CONTACT: Morton, C. C.
Departments of Pathology and Obstetrics, Gynecology and Reproductive Biology
Brigham and Women's Hospital
75 Francis Street, Harvard Medical School, Boston, MA 02115, USA
Tel: 617 732 7980
Fax: 617 738 6996
Email: cmorton@rics.bwh.harvard.edu
DNA sequencing and analyses were performed by National Institutes of Health Intramural Sequencing Center (NISC; see <http://www.nisc.nih.gov>).
This clone is available royalty-free through LIND; contact the IMAGE Consortium (info@image.llnl.gov) for further information.
Plate: LHM6182 row: D column: 19
Seq primer: M13RPI reverse primer (ABI).
Location/Qualifiers
1. 351
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone="IMAGE:2484450"
/tissue_type="cochlea"
/dev_stage="16-22 week fetus"
/lab_host="SOLR cells (kanamycin resistant)"
/note="Organ: ear; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoI; Reference: Genomcs 23, 42-50 (1994) Cloned unidirectionally. Primer: Oligo dT. Fetal cochlea, normal. 37% of inserts <0.5 kb, 56% 0.5-1.0 kb, 7% >1 kb. Uni-ZAP XR Vector. Library constructed by N. Robertson, C. Morton. -5' adaptor sequence: 5' CAAATTCGACACAG 3' -3' adaptor sequence: 5' CTCAGTTTATTTTTTTTTT 3."

ORIGIN
Query Match 100.0%; Score 73; DB 9; Length 351;
Best Local Similarity 100.0%; Pred. No. 0.0046;
Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 AACGTTTATGTTGTTTAAATTATTTATTAAGATGATTCAGATATTATATTTT 60
DB 275 AACGTTTATGTTGTTTAAATTATTTATTAAGATGATTCAGATATTATATTTT 334
QY 61 ATTTATTTTTTT 73
DB 335 ATTTATTTTTTT 347

RESULT 15
LOCUS CB068681 352 bp mRNA linear EST 21-JAN-2003
DEFINITION 1831d11.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6553989 3', mRNA sequence.
ACCESSION CB068681
VERSION CB068681.1 GI:27813201
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE
AUTHORS

1 (bases 1 to 352)

Melton, D., Brown, J., Kenty, G., Permut, A., Lee, C., Kaestner, K.,
Lemshka, I., Scence, M., Brestelli, J., Gradwohl, G., Clifton, S.,
Hiller, L., Marz, M., Page, D., Wylie, T., Martin, J., Bliscain, A.,
Schmitt, A., Theising, B., Ritzer, E., Ronko, I., Bennett, J.,
Cardenas, M., Gibbons, M., McCann, R., Cole, R., Tsagarelshvili, R.,
Williams, T., Jackson, Y. and Bowers, Y.

TITLE
JOURNAL
COMMENT

Unpublished (2000)

Endocrine Pancreas Consortium

Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue

Endocrine Pancreas Consortium

Harvard University, Howard Hughes Medical Institute
Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
MA 02138

Tel: 617-495-1812

Fax: 617-495-8557

Email: dmelton@biohp.harvard.edu

Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
Washington University Genome Sequencing Center For information on
obtaining a clone please contact: Dr. Hiroshi Inoue

(hinoue@im.wustl.edu)

Seq primer: -40RP from Gibco

High quality sequence stop: 322.

Location/Qualifiers

FEATURES
Source

1..352

/organism="Homo sapiens"

/mol_type="mRNA"

/db_xref="taxon:9606"

/clone="IMAGE:6553989"

/tissue_type="Purified pancreatic islet"

/lab_host="DH10B"

/clone_id="HR85 islet"

/note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
Size-selected on agarose gel. Average insert size -1kb. 5'XhoI site was destroyed after directional cloning.
Amplified once. Contact information: Hiroshi Inoue, MD,
Metabolism Div. (Alan Permut Lab), Washington University
School of Medicine, Box 8127, 660 South Euclid Ave., St.
Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
314-362-1916, Fax: 314-747-2692."

ORIGIN

Query Match 100.0%; Score 73; DB 14; Length 352;

Best Local Similarity 100.0%; Pred. No. 0.0046;

Matches 73; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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          |||||
Db      197 AACGTTATTGCTTTTAAATTTATTTATTTATTAAGATGATCTCAGATATTATATTTT 138

Oy      61 ATTTATTTT 73
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Db      137 ATTTATTTT 125

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